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             nucleic search,
 February
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7,
                                GenCore
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2003,
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Title:
Perfect score:
Sequence: 803 US-09-687-837-1\_COPY\_3800\_4300 501 1 caattta+~~~~ 06:53:49; Search time 1010.34 Seconds (without alignments) 8030.908 Million cell updates/sec

Scoring table: IDENTITY\_NUC Gapop 10.0 , ....ttgtgtcttaacaaaggtgt

501

Gapext

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Minimum Maximum DB DB seq length: seq length: 0 20000000000

Total number

of

hits satisfying chosen parameters:

32308132

16154066 seqs, 8097743376

residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database EST:\*

1: em

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	σ	ហ	4	ω	۵	μ	ult No.
	437.2	479	479.8	483	483	489	Score
		95.6	•			97.6	Query Match L
	801	920	644	777	695	835	Length D
	13	12	10	13	9		DB
	BI603180	BG676871	AW162535	BI602169	AL133724	AF188523	ID
	BI603180 603249824	BG676871 602623473	AW162535 au77b01.x	BI602169 603246290	AL133724 DKFZp761J	AF188523 AF188523	Description

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NNO 174	E699344 RC3-NN00	W227478 up10h03.	E930535 RC6-GN00	W463757 BP230013	70666 AL570666	F041935 BP250006	03019 FB20D6 Fet	E703924 MR0-NN	F695548 60185195	1337284 AR088C04	879884 vw01c06.	553184 AL55318	V720937 AV7209	Q694790 1000933	F042085 BP250013.	I050739 RC6-GN	083157 AU083157	W484613 61734 MA	1153873 60287087	044659 BP25002	G468527 60251030	E372746 60122425	G384511 303736 м	I372817 EST17536	A151055 zl45c03.	705585 ab42b01.	в309170 вв30917	372818 EST17536	125739 6024920	G992490 MR3-HT10	484945 aa41b06.r	M353362 iq46a10	353207 ig44a10.	F667219 60212101	53240 EST3653	F748808 MR0-BN01	

## ALIGNMENTS

source	FEATOKES			COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	RESULT 1 AF188523/c
/organism="Homo sapiens" /db_xref="taxon:9606" /clone="ISG 4" /clone_lib="Homo sapiens ATCC HTB-12; SW1088"	Location/Qualifiers	Pennsylvania State University College of Medicine 500 University Drive, Hershey, PA 17033, USA library screened by SSH and reverse Northern blot; increased expression in iron loading was confirmed by Northern blot.	Neuroscience and Anatomy	Contact: Ye Z	Libraries from SSH with Antisense Probe from Three Iron Conditions Unpublished (2000)	Genes by Rescreeni	Ye, Z. and Connor, J.R.	1 (bases 1 to 835)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	etazoa; Chordata;	Homo sapiens	human.	EST.	AF188523.1 GI:7144569	AF188523	•	AF188523 Homo sapiens ATCC HTB-12; SW1088 Homo sapiens cDNA clone	

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Contact: Poustka A.J.

Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analys
Research Center (DKFZ).
                                                                                   Mammalia; Eutheria; Pr
1 (bases 1 to 695)
Poustka, A., Klein, M., 1
EST (Poustka, et al.)
Unpublished (1999)
Contact: Poustra
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/cell_line="ATCC HTB-12; S'
/note="Organ: liver"
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No sl sequence available.

This clone (DKFZp761J19121) is available at the RZPD in Be Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                              316
                                                 NA sequence.
02169
02169.1 GI:
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/lab_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.
cDNA Library Preparation: Michael J. Brownstei
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consor
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at
http://image.llnl.gov
Plate: LLAM11729 row: d column: 24
High quality ~~~~
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                                             CTTTCTATAGGAGTTGTAAGAAGGTGCACATATTTTTTAAATCTCACTGGCAATATTCA
AAGTTTTCATTGTGTCTTAACAAAGGTGT
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Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens
/db_xref="taxon:9606"
/clone="IMAGE:5288423"
/clone_lib="NIH_MGC_96"
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98.4%;
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.2e-115;
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Brownstein
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RESULT 4
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                                                     CAGCTCGAGTATCAGGAAGAAATGAAAGCCAACTACAGGGAAATGGCGAAGGAGCTTTCT
                                         Homo sapiens
Eukaryota; Metazoa; Choroacu,
Mammalia; Eutheria; Primates; Catarrhini, ...

1 (bases 1 to 644)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
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AW162535.1
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High quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone is available royalty-free through LLNL; E Consortium (info@image.llnl.gov) for further ible reversed clone: polyT not found primer: -40UP from Gibco
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                                                                                              Conservative
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                                                                                                                                                            /note="Organ: brain; Vector: pBlusite_1: SstI; Site_2: XhoI; Doubl prepared from human fetal brain tadaptors were used in cloning as
                                                                                                                                                                                                                                                                                    /sex="male"
/tissue_type
                                                                                                                                                                                                                                                                                                                                                                                                                             /oryanism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2782249"
                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Schneider fetal brain 00004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 bp mRNA linear EST 09-NOV Schneider fetal brain 00004 Homo sapiens cDNA clone 249 3' similar to TR:Q63603 Q63603 TRG MRNA;, mRNA
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98.0%;
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                                                                                                         Score 479.8; DB 10; Pred. No. 8.3e-115;
                                                                                                                                                                                                                                                                                                                           brain; Vector: pBluescript SK (Stratagene);
Site_2: XhoI; Double-stranded cDNA was
human fetal brain tissue. 5' and 3'
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                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectic Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10600 row: a column: 19
High quality sequence stop: 849.
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EST.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
1 (bases 1 to 920)
            274
                                                                                                                                                                             e: LLAM10600 row: a column: quality sequence stop: 849. Location/Qualifiers
  /organism="Homo sapiens"
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/clone="IMAGE:4748442"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: No. Site_2: SalI; Cloned unidirectionally. Primer: Olivaverage insert size 1.5kb. Library constructed by Technologies. Note: this is a NCI_CGAP_Library."
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                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shingshipuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                        rucyte Gen found through the I.M.A.G.E. Conty, the found through the I.M.A.G.E. Conty, finage.llnl.gov
Plate: LLAM11763 row: r
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603249
mRNA 5
BI6031
BI6031
EST.
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249824F1 NIH_MGC_96 Homo sapiens cDNA clone
A sequence.
03180
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Location/Qualifiers
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larity 98.6%;
Conservative
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          ′organism="Homo
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ganism="Homo sapiens
_xref="taxon:9606"
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Pred. No. 1.4e-114;
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Local Similarity 96.3%;
nes 493; Conservative
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                                                         Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 546)
Dias Neto, E., Garcia
 Nagai, M.A., da
Goldman, G.H.,
Brunstein, A.,
                                                                                                                                                                                                                                                                    BF748808
MR0-BN0115-041000-013-e10
BF748808
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/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: SalI-XhoI (gtcgag pBluescript KS+); SalI-XhoI (gtcgag pBluescript KS+); Site_1: SalI-XhoI (gtcgag pBluescript KS+); Site_1: SalI
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., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., ., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                    GI:12075471
                                                                                                                          Chordata; Craniata; Vo
Primates; Catarrhini;
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i; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-BN0115-
041000-013-e10&t3=2000-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 545.
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Proc. Natl. Ac
20202663
Contact: Simps
Laboratory of
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n quality sequence start: 16
n quality sequence stop: 545.
Location/Qualifiers
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gun sequencing of the human transcriptome with ORF
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 GTGTCTTAACAAAGGTGT
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Institute for Cancer Research
of. Antonio Prudente 109, 4 and
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/clone_lib="BN0115"
/dev_stage="Adult"
/note="Organ: breast_norma.
Site_2: SmaI; A mini-libra.
derived from Opposition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo
/db_xref="+---
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99.1%;
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Pred. No. 4.5e-101;
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Best Local Similarity 97.5%;
Matches 430; Conservative
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Quackenbush, J.
Assessment of gene expression patterns in metastasis using a 19,200 element cDNA mi Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20 Tel: 301 838 3528
Fax: 301 838 0208
Email: johng@tigr.org
                                                                                                                                                                                                GAAATCATGCATGAGCA-----GATCTGCCCCCTGGAGGAGAAGACGAGCGTCTTAC
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                                      GGGAGGACCAAGGGGAAGGGAGAGAAAGAAATAAAGAACAACGTTATTTCTTAACAGA
                                                                                                                    GGATGACCAGCTCGTCTTCGGTCGTGTGATTACATCTCATGGCCCGTGTGTGGGGACTTG
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
146 c 191 g 147 t
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Catarrhini; Hominidae;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MG Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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602121018F1 NIH_MGC_56 Homo
mRNA sequence.
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ional Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4278077"
/clone="Iib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5;
and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5;-CACGGCCATTATGGCC-3; and 3; adaptor
sequence: 5;-CATGCTAGAGGCCGACGCGCCACATG-dT(30)BN-3;
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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1 to 574)
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/db_xref="taxon:9606"
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Pred. No. 4.2e-90;
); Mismatches 3;
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Endocrine Pancreas Consortium

Unpublished (2000)
Other_ESTs: ig44al0.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                             CAGCTCGAGTATCAGGAAGAAATGAAAGCCAACTACAGGGAAATGGCGAAGGAGCTTTCT
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Eukaryota; Me
Mammalia; Eut
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Library was constructed by Dr. Hiroshi Inoue DNA sec
Washington University Genome Sequencing Center For obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
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malia; Eutheria;
(bases 1 to 521)
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Location/Qualifiers
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                                                                                                                                                                                        /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5 XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Homo sapiens cL
mRNA sequence.
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                                                                                                   Score 369; DB 13;
Pred. No. 7.1e-86;
); Mismatches 0;
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Mammalia; E
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BM353362.1
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ig46a10.y1
Q63603 TRG
                                                                                                                                                                                                                           Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 478.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dept
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Email
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Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                           02
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617-495-8557
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/db_xref="taxon:9606"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 bp mRNA
HR85 islet Homo sapiens cDNA 5'
PROTEIN ;, mRNA sequence.
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         noue, MD,
University
Ave., St.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridge,
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Mammalia; Eutheria; Primates; Catarrhini; Homin
1 (bases 1 to 359)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatom
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.B
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCTCGAGTATCAGGAAGAAATGAAAGCCAACTACAGGGAAATGGCGAAGGAGCTTTCT
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il Similarity 99.7%;
368; Conservative
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aa41b06.rl
similar to
AA484945
AA484945.l
                                                         cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 rev1 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                               Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                    human
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/organism="Homo sapiens
/db_xref="GDB:6035413"
/db_xref="taxon:9606"
/clone="IMAGE:815795"
                                                                                                                                                                                                                                                                                                                                                                                                    359 bp mRNA NCI_CGAP_GCB1 Homo sapiens cDN. TR:G550420 G550420 TRG MRNA;
                                                                                                                                                                                                                                                                                                                                                                             GI:2214164
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Pred. No. 1.3e-85;
0; Mismatches 1;
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ens cDNA clone IMAGE:
MRNA ;, mRNA sequence
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IMAGE:815795 5'
                                                                                                                      Sequencing (information
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RESULT 13
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Best Local Similarity 100.0%;
Matches 359; Conservative
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E 1 (bases 1 to 609)

S Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

E 20202663

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATTA
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                                                                                                                                                                                                       Homo
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                                                                                                                                                                                                                                         609 bp mRNA linear
HT1039-020201-002-b09 HT1039 Homo sapiens cDNA,
92490
92490.1 GI:14396560
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Pred. No. 2.8e-83;
0; Mismatches 0;
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Local Similarity 97.6%;
es 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsonerung.

This sequence was derived from the fine project. This entry can be seen in the (http://www.ludwig.org.br/scripts/get020201-002-b09&t3=2001-02-02&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 6

High quality sequence stop: 605.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTCGTCTTCGGTCGTGTGATTACATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                            CTTCACATCTTCAACGCCATCAGTGGGACTCCAACAAGCACAATGGTTCACGGGATGACC
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                                                                                                                                                                                                                                                                                                                                                                               CTTCACATCTTCAACGCCATCAGTGGGACTCCNACAAGCACAATGGTTCACGGGATGACC
                                                                                                                 BG425739
602492044F1 NIH_MGC_
mRNA sequence.
BG425739
BG425739.1 GI:13332:
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhini
1 (bases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                     human.
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Brazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prof.
zil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           þ
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Site_2: Smal;
derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

160 c 157 g 158 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone_lib="HT1039"
/dev stare=""
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                                                        Craniata; Vertebrata; Catarrhini; Hominidae
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1344 row: g column: 11
High quality sequence stop: 617.
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AGGTGCA
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EST175362 Infant brain, I
FUHIBU1, mRNA sequence.
AI372818
AI372818.1 GI:4152684
EST.
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ne distribution: MGC clone distribution information can be
d through the I.M.A.G.E. Consortium/LLNL at:
://image.llnl.gov
e: LLCM1344 row: g column: 11
quality sequence stop: 617.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4606114"
/clone=lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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Pred. No. 4.3e-68;
0; Mismatches 10;
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S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

(C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

(O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

(L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Palligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

N.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and

Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

NE 90705280

Other_ESTs: EST175338 EST175335 EST175331 EST175332

EST175339 EST17534 EST175325 EST175336 EST175337 EST175338

EST175339 EST17534 EST175335 EST175336 EST175337 EST175338

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84; Conservative
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/db_xref="taxon:9606"
/clone="FUHIBU1"
/clone=lib="Infant brain, Bento Soares"
/clone_lib="Infant brain, Bento Soares"
/lab_host="E. coli DH5-alpha"
/note="Vector: BA, M13-derived; Site_1: HindIII; Site_2:
NotI; The infant brain library, constructed by Bento
Soares, Columbia University, was oligo-(dT) primed and
directionally cloned into an M13-derived plasmid using
total brain mRNA from a 72-day old human female afflicted
with spinal muscular atrophy. "
1 others
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Catarrhini; Hominidae;
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## SUMMARIES

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//Product="zizinin1"
//protein_id="AAM90306.1"
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//protein_id="MSOPPLLPASAETRKFTRALSKPGTAAELROSVSEVVRGSVLLA
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KDEDAASLGGOKGGITKHGWLYKGNMUSAISVTMASFKKRFFHLIQLGDGSYNLNFYK
DEKISKEPKGSIFLDSCMGVVONKVRRFAFELKMQDKSSYLLAADSEVEMEEMITIL
NKILOLNFESAAMOEKRNGDSHEDDEOSKLEGSGSGLDSYPELAKKSARRAEIKLKSES
RVKLFYLDPDAGKLDFSSAEPEVKSFEEKFGKRILVKCNDLSFNLQCCVAENEEGFT
NVEPFFVTLSLEDIKYNKISADHFVVDLNHFSVRQMLATTSPALMNGSGOSPSYLKGI
LHEAAMOYEKROGIFSVTCHHPDIFLVARIEKVLQGSITHCABEYMKSSDSSKVAQKVL
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FVPCIFKHTOPYTIYNHLYVYPKYLKYDSOKSFAKARNIAICIEFKDSDEEDSOPLK
CIYGRPGGPVFTRSAFAAVLHHHQMFFFYDELK IELPYQALLPSGYLCYGELGMCHYG
PEIKWVDGGKPLLKISTHLVSTVYTQDOHLHNEFGYCGKTESGAQALGNELVKYLKSL
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VKYAYKAAEPYVASEXTYTHEELTKSWTTILKPSADEITSNKLLKYSWFFFDLLIKSH
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AUNILVTOPKOSTLDNSTLTBEFGRHFITGLLLREVGTYLQEFRVVCNHEHYIPALNLPMPFG
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KRCFTFWDRGFVEKGILNHOSTIGNSTARNSTTSTPURSHARROGLASHLSTDSG
NSLPERNSEKGNSLDKHOOSSTIGNSVTCOKTESGADCHARNINGVRNABSRGSLISTDSG
NSLPERNSEKGNSLDKHOOSSTIGNSVTCOKTESTTSTPURSHARROGLASHINKRYFDVF
KGSTLANDVLHQSTLARNNFDYTGKKSFVRTHLQVILSFTTLAFKYKHELLACKONSKLSIR
PELKKTWLDSHARIHTSFSSDVKDLTKRETSTFTETEGRADCAALCYEILKCCNSKLSSIR
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ANFFOCAAQYOFTDSETDVEGFFEDEDGKEYIYKEPKLTFENGERCHLARYFREGS
ENVKMTOLSSHARAHDTILSKARDEERLAHLTDTLHRASTYTTKREANVQMEPPLLPHSHSA
CLRRSGGGVFRQGCTAFRVITTNIDEBASMMEDVGMODVHFNEDDVLKELLEQCADGLW
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/chromosome="13"
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PFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKK
VAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKRYPDNKVKLL
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AB028981.2 G
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Mammalia; F
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Submitted (17-JUN-1999)
Laboratory of DNA Technology
Techno
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Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.
Prediction of the coding sequences of unidentified
XIV. The complete sequences of 100 new cDNA clones
code for large proteins in vitro
DNA Res. 6 (3), 197-205 (1999)
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1. .7545
/codon_start=1
/product="KIAA1058 protein"
/protein_id="BAA83010.2"
/db_xref="GI:20521746"
/translation="LACLCLARPGTRSCSSCRLSDLRFQPRMQADKCRTSSRSVKKEL
VIESPLQYKDAAQGEVEAESPGPVPAKPKLIEPLDYENVIVQKKTQILNDCLREMLLF
PYDDFQTAILRRQGRYICSTVPAKAEEEAQSLFVTECIKTYNSDWHLVNYKYEDYSGE
FRQLPNKVVKLDKLPVHVYEVDEEVDKDEDAASLGSQKGGITKHGWLYKGNMNSAISV
TMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPKGSIFLDSCMGVVQNNKVRRFAFE
LKMQDKSSYLLAADSEVEMEEWITILNKILQLNFEAAMQEKRNGDSHEDDEQSKLEGS
                                                                                                                                                                                                                                                                         /gene="KIAA1058"
<1. .6280
                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained bysubcloning of fragments derived from two cDNA clones (1 - 1846 derived from ef00877 and 1847 - 7545 was derived hhl2146)."
                                                                                                                                                                                                                                                                                                                                               hh12146).
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/db_xref="taxon:9606"
/chromosome="13"
/clone="hh12146s1"
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Japan (E-mail:cdnainfo@kazusa.or.jp,
18-52-3914)
2002 this sequence
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                   CCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGTCTGCATGCGATGGA
                                                                                   ATGGGTAGATGGAGGCAAGCCACTGCTGAAAAFTTTCCACTCATCTGGTTTCTAC
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QHIPVSANLPSGYLGYQELGMGRHYGPEIKWVDGKPLLKISTHLVSTVYTQDQHLHN
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VNVTRVIIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKP
SADFLTSNKLLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQFFVASYHHAVETVVNML
MPHITQKFRDNPEASKNANHSLAVFIKRCFTEMDRGFVFKQINNYISCFAPGDPKTLF
EYGFALQEFREVRLIAISVLKNLLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQ
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YTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDK
LDQSEIKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRY
LDQSEIKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRY
EGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRRNNFDYTGKKSFVRTHLQVII
SVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRLIYKFPSTFY
EGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRRNNFDYTGKKSFVRTHLQVII
SVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATA
QMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVT
ALVAEYLTRKEAVQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMME
DVGMQDVHFNEDLVHMSKRYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVT
THRAXYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYI
YKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPF
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GPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEE
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RILVKCNDLSFNLQCCVAENEEGPTTNVEPFFVTLSLFDIKYNRKISADFHVDLNHFS
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KIELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTS
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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.3; Conserva
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//COUCH_SCALL=1
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//EDCHALL 1.14 59 9 79 76 "
//ED_XIFEF=1GI:14 59 9 76 "
//EDAKRAQSLFVKECIKTYS
//LTAINS 1 at 1.01 = "MEPMEDISISVIGRORRTVOSTVPEDAEKRAQSLFVKECIKTYS
//TURNORY KYEDESGDERKLENCKSLERPEKIPHLYFELDEDCEKDEDSSSLCSQKGGVI
KQGNLHKANVNSTITVTMKYFKRRYFLITOLDGSYILNSYKDEKNSKESKGCIYLDA
CIDWYOCPKMRRHAFELKMLDKYSHYLAAETEDGMEEMLITLKKIIQINNDSLYQEKK
ETVETAQDDETSSQGKAENIMASLERSHIPELMKYGRETEQLMKLSRSDGRONLESED
LRYIQOGIFSVTNHHPEIFLVAR TEKVLOGNITHGAEPYIKNSDFWRAQKYHRTAKO
CLOVVOCPKMRRHAPEIFLVAR TEKVLOGNITHGAEPYIKNSDFWRAQKYHRTAKO
LRYIQOGIFSVTNHHPEIFLVAR TEKVLOGNITHGAEPYIKNSDFWRAQKYHRTAKO
VCSRLGGYIRNFAMAARPIFKDTOGSLDLDGRRSPLYKOGDSSLSSEDIKKLLSEYKK
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PKTKLQIIFOGLUNITURCVPVDLSNCITSSYVPLKPFEKNCONITYEVEEPEYPEMTK
YCYPFTIYKHHLYYYPLQLKYDSGKTFAKARNIAVCVEFEDSDESDASALKCIYGKRA
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GSVFTTNAAAVVSHHNQNPEFYDEIK IELPIHHOKHHLLTFYFYHYSCEIMYKKY
PKTKYST
GSKPLLKFKSHLESTIYTODLHYWKFFHICQLIQSGSKEVPGELIKIKKCLHAMEIQV
MIGFLPVILMQLERYLTMNTHEDDUP INCTMVLLH YSKCHEEGLDSYLKRSIKYSF
KYCYPFTIYNAAVAVSHHNQNPEFYDDEILITATSIAIN SKAPTYLLEE
NKIKLPRQORFPETYHHVLHSLLLAIIPHYTIKAEIPDESRNVNYSLASFIKKCLHAMEIQV
MIGFLPVILMGLERYLTMTMIALLXGSADFJSINKLLKYSMFFFEIL IKKNCHAMPAKPKLOR
QRKRICHTHYLLTATMIAILKGSADFJSINKLLKYSMFFFEIL IKKNCHAMPAKPKLOR
RGSLSTDKOTAYGSFOKDFKVLAEKKFFFLOGNTIGNETRYTAISYIKHLLIKHAFDIR
YQHKNQOAKIAQUKTLESTIYLDTISSGSTROONTERTYTAISYIKKLLIKHAFDIR
YGHKNQOAKIAQUKTLESTYLLLERTSISLALDNUSIRSTRYTAISYIKLLIKHAFDIR
YGHKNQOAKIAQUKTLESTYLTDTISSGSTROONTERTSYSSYS
QXNRLDQVEIRSLLMKCYLIYFTWMKYSPOELINILLIKYOLTHRYNA
GKRNIARHYNSALEGYTAKSTELLTYFWNKYSPOELINILLIKYOLTHRYNA
RGSLSCHAHPARAKYTOLTYTWMXSPOELINILLIKYOLTHRYNA
RGSLSCHAHPARAKYTOLTYTWMXSPOELINILLOQUSTATSXSTREPE
KTWALOSAAKIHVKNGDSEAANCYHVAATAGATATKKLFPNCGSAFKKITPNUDE
KTWALOSAAKIHVKNGDSEAANCYHVYANAAELDAFYTATSNSTRUNDAYARA
VKELSDIHHOLISGT
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/db_xref="taxon:9606"
/note="full length human
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Primates;
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Assembly program: |
Quality coverage:
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Direct Submission

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BP 191 91006 EVRY
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                      Heilig, R., Petit, J.L., Vico, V., Dasilva Brottier, P., Cattolico, L., Barbe, V., Pe Levy, M., Eckenberg, R., Bruls, T., deBera Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14
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                                                                                                                          Center: Genoscope / Centre National de
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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Human chromosome 14 DNA sequence BAC C-2373J19 of library CalTech-D
from chromosome 14 of Homo sapiens (Human), complete sequence.
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                                                         following BAC sequence is oriented from the T7 to the SP6 cream BAC (overlapping the T7 end): R-857B24 (AC=AL049870) stream BAC (overlapping the SP6 end): R-398E10 ------
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                                                mary Statistics
                                                                                                                                                                                                                           nitted (26-APR-2001) Genoscope - Centre National de Sequencage
91 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
b : www.genoscope.cns.fr)
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8.87x in
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Barbe,V., Pelletier,E., Artiguena
ls,T., deBerardinis,V., Cruaud,C.,
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ier,E., Artiguenave,
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sequence from clone RP11-155N3 on chromosome 13
s and GSSs. Contains the 3' part of a novel gene
94, the KIAA1058 gene and a putative novel gene,
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13

Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl3

This sequence is the entire insert of clone Rp11-155N3 The true left end of clone Rp11-318G11 is at 114983 in this sequence. The true right end of clone Rp11-56D6 is at 42341 in this sequence. The true right end of clone Rp11-55M18 is at 43464 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements, where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

RP11-155N3 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 163316)

S Smith, M.

Direct Submission

L Submitted (31-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 1, 2000 this sequence version replaced gi:10039689.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission variation annotation may not be found in the sequence submission
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QHLSSLESSFTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCFKTHFLN
NDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFC
YEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVAL
SGGSRFQESLFIINNFANSDRPMLARAFPAEVKDLTKRIRTVLMATAQMKEHEKDPEM
LIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHVAALVAEFLHRKK
LFPNGCSAFKKITPNIDEEGAMKEDAGMMDVHYSEEVLLELLEQCVNGLWKAERYEII
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SRNVNYSLASFLKCCLTLMDRGFVFNLINDYISGFSPKDPKVLAEYKFEFLQTICNHE
HYIPLNLPMAFAKPKLQRVQDSNLEYSLSDEYCKHHFLVGLLLRETSIALQDNYEIRY
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1 (bases 1 to 4393)

Lu,P., Garman,J.D. and Candia,A.F.

Clasp-4 transmembrane protein

Patent: WO 0142294-A 97 14-JUN-2001

Arbor Vita Corporation (US)

Location/Qualifiers
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Direct Submission
Submitted (09-FEB-2002) Human Genome Sequencing Center, Depair of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 175281)
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_c
NOTE: This is a 'working draft' sequence. It currently
consists of 75 contigs. The true order of the pieces
is not known and their order in this sequence record is
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n,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
eland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.
la,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Direct Submission
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Cleveland, C.D.,
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Center clone name: CH230-473M19
Center clone name: CH230-473M19
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 10
Assembly program: Phrap; version 0.99
Consensus quality: 117932 bases at leconsensus quality: 124308 bases at leconsensus quality: 124308 bases at leconsensus quality: 129203 bases at leco
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 89 contigs. The true order of the pieces is not known and their order in this sequence record is
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human cDNA sequencing project supported by Ministry of human cDNA sequencing project supported by Ministry of and one pass sequencing: Research Association for Biotechnology; alibrary construction and clone selection: Kazusa DNA Research
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Homo sapiens
AK090429
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NEDO human cDNA sequencing project s
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Jikuya, H., Takano, J., Kikuno, R.,
Direct Submission
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INCCLTPEMLPVKPFPENRTRPHKEILEFPTREVYVPHTVYRNLLYVYPQRLNFVNKL
ASARNITIKIQFMCGEDASNAMPVIFGKSSGPEFLQEVYTAVTYHNKSPDFYEEVKIK
LPAKLTVNHHLLFTFYHISCQQKQGASVETLLGYSWLPILLNERLQTGSYCLPVALEK
LPPNYSMHSAEKVPLQNPPIKWAEGHKGVFNIEVQAVSSVHTQDNHLEKFFTLCHSLE
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                                                                                                                                                                                                                                                 /gene
                                                                                                                                                                                              /note="Start codon
/codon_start=2
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'clone="FLJ00346"
'tissue_tvro-"
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Eutheria;
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/gene="FLJ00346"
                                                                                                                                                                                                                                                                                          note="vector:pBluescriptII"
                                                                                                                                                                                                                                                                                                          /tissue_type="spleen
/dev_stage="adult"
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  (E-mail:cdnainfo@kazusa.or.jp,
   Tel:81-438-52-3913,
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EOVERNTULTTMHAEFDVIKTBETGVICKFEFEVITTBETENATERFYTTLEGRPRGELH
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DAKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGE
AVEKNKRLITADQREYQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFH
RSSFRKCETQLSQGS"
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          ACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGTCA 408
                               CCACCCAACTACTCCATGCATTCTGCTGAGAAAGTCCCATTACAGAATCCTCCC
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AX174569
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             REFERENC
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                                                    ORGANISM
                                                                                      AX174569
Sequence 1
AX174569
AX174569.1
  Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 7215)
Lu,P., Garman,J.D. and Candia
                                                                 huma
                                                                                                               7215 bp from Patent W00142296.
                                                                                      GI:14598200
and Candia,
                       Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                           DNA
                        Hominidae;
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                                    Euteleostomi;
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Matches 208; Conser
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ELDPHVRDCVQTYIREWLIVNRKNQGSPEICGFKKTGSRKDFHKTLPKQTFESETLEC
SEPAAQAGPRHLNVLCDVSGKGPVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEE
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YIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQGSVGAT
VNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQREY
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/protein_id="CAC43733.1"
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L Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp66701117) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is availa
at http://mips.gsf.de/proj/cDNA/.

Location/Qualifiers
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PR 114 14-APR-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; LT 1 7972 AAC87972 CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective; hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis; endommetriosis; pregnancy induced hypertension; ss. Human Homo 07-MAR-2001 AAC87972; 13-APR-19-OCT-WO200061747 sapiens. CLASP 2000 2000 st andard; -A2. -2 nucleotide sequence. (first entry) 2000WO-US10158 99US-0129171. 99US-0134114. 99US-0134117. 99US-0134118. CDNA; 4807 BP.

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antianaemic, haemostatic and neuroprotective activities with the used to inhibit an immune response in a subject by interfering with the ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat

The present invention describes caumerin time asymmunomodulatory, (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be antianaemic, haemostatic and neuroprotective activities.

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                 Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation; CLASP; gene; ss.
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                                                                               is, autoimmune thyroiditis, and autoimmune pulmonary n. CLASP-2 can be used to treat anaphylaxis or ivity to an antigenic molecules, organ rejection or graft-disease (GVHD) and inflammation. ABK84922-ABK85018 adherin-like asymmetry protein (CLASP) coding sequences and
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Example 4; Figure 6A; 245pp; English.

The invention relates to an isolated polypeptide (I) comprising an amino cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, 2E)
CC cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, 2E)
CC sequences (PS). (I) is useful for identifying a compound or agent that to binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for detecting a clasp-2 polypeptide in a sample. (II) is useful for comprising a immune response in a subject. A pharmaceutical composition comprising a nucleic acid encoding (I), or (II) is useful for preventing correcting a clasp-2 polypeptide in a sample. (II) is useful for preventing comprising a nucleic acid encoding (I), or (II) is useful for preventing correction or inhibition of clasp-2 asyression (e.g., antisense or ribozyme-mediated inhibition), for gene knockout, etc. The CLASP-2 polypurelectides are useful as probes or primers for clasp-2 polypurelectides can be used in diagnostics (e.g., as probes for CLASP-2 polypurelectides. The CLASP-2 polypurelectides can be used in diagnostics (e.g., as probes for CLASP-2 polypurelectides can construct transgenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polypurelectides can construct transgenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polypeptides or polynuclectides can treat deficiencies or disorders of the immune system, by activating or inhibiting the activation, differentiation of immune cells and can treat or detect deficiencies or disorders of haematopoietic cells. CLASP-2 polypeptides can increase differentiation and proliferation of haematopoietic cells. CLASP-2 polypeptides can increase in certain (or many) types of haematopoietic cells, including the pluripotent stem cells to treat those disorders associated with a decrease in certain (or many) types of haematopoietic cells e.g., amandiated and plectasia, common variable inmune cells of the contraction of the contraction of the contraction of the contraction of the hypersensitiversus-host orepresent can and PCR prima immunodeficiency, Digeorge syndrome, lymphopenia, thrombocytopenia, or haemoglobinuria). CLASP-2 polynucleotides or polypeptides can treat or detect autoimmune diseases, e.g., Addison's disease, haemolytic anaemia Grave's disease, multiple sclerosis, rheumatoid arthritis, lupus, endometriosis, autoimmune thyroiditis, and autoimmune pulmonary inflammation. CLASP-2 can be used to treat anaphylaxis or Sequençe nsitivity to an antigenic molecules, organ rejection or graftnost disease (GVHD) and inflammation. ABK84922-ABK85018 at cadherin-like asymmetry protein (CLASP) coding sequences primers of the invention. 807 BP; 1353 A; 1117 C; 1136 G; 1201 T; 0 other;

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The invention relates to an isolated polypeptide (I) comprising an amino acid sequence that has 90 % sequence identity to one of the human cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, 2E) sequences (PS). (I) is useful for identifying a compound or agent that binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for detecting a CLASP-2 polypeptide in a sample. (II) is useful for inhibiting a immune response in a subject. A pharmaceutical composition comprising a nucleic acid encoding (I), or (II) is useful for preventing
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499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    itivity to an antigenic molecules, organ rejection or graft-st disease (GVHD) and inflammation. ABK84922-ABK85018 cadherin-like asymmetry protein (CLASP) coding sequences and rs of the invention.
                                        TGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTACA
                                                                                                                                                                                                                             GTGATGATCGCCT
                                                                                                       ACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGTCAGAAAACCGAATCT
                                                                                                                                    ACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGTCAGAAAACCGAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity
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disease is caused or exacerbated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 499; DB 24;
100.0%; Pred. No. 6.7e-157;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4806;
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481

GGCCACGTGATGATCGCCT

499

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RESULT 6
ABK84965
ABK84965
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ACX ABK8
ACX
                                                                                                                 CC acid sequence that has 90 % sequence identity to one of the human CC acid sequences that has 90 % sequence identity to one of the human CC cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, ZB, ZC, ZE) compenses (PS). (I) is useful for identifying a compound or agent that CC binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for CC detecting a CLASP-2 polypeptide in a sample. (II) is useful for CC inhibiting a immune response in a subject. A pharmaceutical composition CC comprising a nucleic acid encoding (I), or (II) is useful for CC comprising a nucleic acid encoding (I), or (II) is useful for preventing or treating a CLASP-2 mediated disease e.g. an autoimmune disease, where the autoimmune disease is caused or exacerbated by increased activity C of TH1 cells. CLASP-2 polynuclectides are useful as probes or primers for CLASP-2 mediated inhibition), for gene knockout, etc. The CLASP-2 C polynucleotides can express CLASP-2 polypeptides, produce anti-CLASP-2 polynucleotides can be used in diagnostics (e.g., as probes CLASP-2 expression), as a lymphocyte marker and for therapeutic colynucleotides can screen for CLASP-2 agonists and antagonists. CLASP-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 colypeptides or polynucleotides can treat deficiencies or clasp-2 colypeptides or polynucleotides can treat deficiencies or clasp-2 clasp-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 clasp-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 clasp-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 clasp-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ARBO-)
(GARM/)
(CAND/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding
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                              CLASP-2 polypeptides or polynucleotides disorders of the immune system, by activation, differentiation of immune condeficiencies or disorders of haematopoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human cadherin-like asymmetry protein(s) (CLASP)-2 for immune response, and for treating multiple sclerosis, arthritis, endometriosis, lupus, autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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)B; ABG61671.
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GARMAN J D.
CANDIA A F.
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                                                         f the immune system, by activation of immune cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Figure
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                                                           leotides can treat deficiencies by activating or inhibiting the
        differentiation and
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RESULT 7
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ID ABK8
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AC ABK8
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DE DNA
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haemoglobinuria).
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                                                                                                                                            tandard; cDNA;
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                                                               cadherin-like asymmetry protein (CLASP) isoform
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0;

Human; blood

prot

autoimmune disease; haematopoietic disorder; Digeorge syndrome; protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; telangiectasia; common variable immunodeficiency; lymphopenia; cytopenia; haemoglobinuria; Addison's disease; Grave's disease;

ataxia

thrombocytopenia;

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Computation a CLASP-2 mediacute or exacerbated by including a CLASP-2 mediacute or exacerbated by including a CLASP-2 mediacute or exacerbated by including a CLASP-2 polynucleotides are useful as probes or primers of the autoimmune disease is caused or expression (e.g., antisense or detection or inhibition of CLASP-2 expression (e.g., antisense or cribozyme-mediated inhibition), for gene knockout, etc. The CLASP-2 complynucleotides can express CLASP-2 polypeptides. The CLASP-2 complynucleotides or are used as therapeutic polypeptides. The CLASP-2 complynucleotide or fragments can be used in diagnostics (e.g., as probes for CLASP-2 expression), as a lymphocyte marker and for therapeutic purposes. CLASP-2 polynucleotides can construct transgenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polynucleotides can screen for CLASP-2 agonists and antagonists. CLASP-2 polynucleotides or polynucleotides can treat deficiencies or disorders of the immune system, by activating or inhibiting the cativation, differentiation of immune cells and can treat or detect deficiencies or disorders of haematopoietic cells. CLASP-2 polypeptides or polynucleotides can increase differentiation and proliferation of haematopoietic cells, including the pluripotent stem cells to treat those of the complex of the pluripotent stem cells to treat those of the complex of the pluripotent stem cells to treat those of the complex of the pluripotent stem cells to treat those of the complex of the complex of the complex of the pluripotent stem cells to treat those of the complex of t
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represent
PCR primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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response, and for treating multiple sclerosis,
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st disease (GVHD) and inflammation. ABK84922-ABK85018
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of
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treating e.g. cancers, proliferative disord
erative disorders and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiogenesis associated protein; AAP; cytostatic; cardiant; gene therapy; ophthalmological; vulnerary; myocardial infarction; macular degeneration; diabetic retinopathy; angiogenesis; wound healing; prophylactic; vaccine; rheumatoid arthritis; psoriasis; drug screening; tumour; transplantation; cancer; therapeutic; diagnostic; human; thyroid regulated transcript;
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                                                     ling cDNA molecules, which are useful for modulating is. AAP proteins and nucleic acids are useful for promoting ling, for example after organ transplantation, and in the of tumours, myocardial infarction, cancers, diabetic in and DNA's are useful in potential prophylactic and ic applications implicated in a variety of disorders including ited to angiogenesis, and also in diagnostic applications.
                                                                                                                                                                                      age 18-21; 159pp; English.
                                                                                                                                                                                                                                                                     602775/68.
                                                                                                                                                                                                                                                                                                                    NENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s also useful in gene therapy. The invention also relates to or screening a tissue sample for tumourigenic potential. AAP re used to screen drugs or compounds that modulate AAP activity ion as well as treating disorders characterised by insufficient ve production of AAP or production of AAP forms that have or aberrant activity compared to the wild type protein, or
                                                                                                                                                                                                                                                                                                                              RAGEN CORP
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                                                                               Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome, blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease, haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation; CLASP; gene; ds.
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CC The invention relates to an isolated polypeptide (I) comprising an amino cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, 2E) cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, 2E) comparising a CLASP-2 polypeptide. An antibody (II) to (I) is useful for detecting a CLASP-2 polypeptide in a sample. (II) is useful for comprising a nucleic acid encoding (I), or (II) is useful for comprising a nucleic acid encoding (I), or (II) is useful for preventing comprising a nucleic acid encoding (I), or (II) is useful for preventing or treating a CLASP-2 mediated disease e.g. an autoimmune disease, where the autoimmune disease is caused or exacerbated by increased activity of TH1 cells. CLASP-2 polynucleotides are useful as probes or primers for detection or inhibition of CLASP-2 expression (e.g., antisense or ribodies or are used as therapeutic polypeptides, produce anti-CLASP-2 polynucleotides can express CLASP-2 polypeptides, produce anti-CLASP-2 polynucleotides or are used as therapeutic polypeptides. The CLASP-2 polynucleotides can be used in diagnostics (e.g., as probes continuals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polypeptides can screen for CLASP-2 agonists and antagonists. CLASP-2 clasp-2 polypeptides or polynucleotides can construct transgenic and knockout clasp-2 polypeptides or polynucleotides can construct transgenic and knockout clasp-2 polypeptides or polynucleotides can construct transgenic and knockout clasp-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 disporters of the immune system, by activating or inhibition the clasp-2 activation or inhibition.
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GARMAN J D.
CANDIA A F.
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                                                                                                                                                                                                                                                                                    in disorders (e.g., agammaglobulinaemia, bulinaemia, ataxia telangiectasia, common variable bulinaemia, ataxia telangiectasia, common variable iency, Digeorge syndrome, lymphopenia, thrombocytopenia, or uria). CLASP-2 polynucleotides or polypeptides can treat or immune diseases, e.g., Addison's disease, haemolytic anaemia, ease, multiple sclerosis, rheumatoid arthritis, lupus, is, autoimmune thyroiditis, and autoimmune pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                         ypeptides or polynucleuring on inhibiting the f the immune system, by activating or inhibiting the differentiation of immune cells and can treat or detect s or disorders of haematopoietic cells. CLASP-2 polypeptides eotides can increase differentiation and proliferation of tic cells, including the pluripotent stem cells to treat those ssociated with a decrease in certain (or many) types of significant immunologic deficiency syndromes including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adherin-like asymmetry protein(s) (CLASP)-2 for modulating esponse, and for treating multiple sclerosis, rheumatoid endometriosis, lupus, autoimmune thyroiditis, septic shock,
ivity to an antigenic molecules, organ rejection or gradisease (GVHD) and inflammation. ABK84922-ABK85018 adherin-like asymmetry protein (CLASP) coding sequences mers of the invention.
                                                                                                                                                                                                                                                     is, autoimmune chyrotature, chasp-2 can be used to treat anaphylaxis
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RESULT 13
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29-OCT-1999;
13-DEC-1999;
14-JAN-2000;
14-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective; hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis; endometriosis; pregnancy induced hypertension; ss.
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                                        99US-0129171.
99US-0134114.
99US-0134117.
99US-0134118.
99US-0160860.
99US-0162498.
99US-0170453.
2000US-0176195.
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Loca

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The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, cantianaemic, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the cability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject by interfering with the cantibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat a CLASP-2 consensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e,g, arthritis, inflammatory bowel disease and increase caneemia, thrombocytopaenia and other blood protein disorders. Disorders treated by disrupting CLASP-2 function include multiple sclerosis, The present sequence represents a preliminary CLASP-2 nucleotide sequence, from the present invention.
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P-PSDB; A/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated cadherin-like asymmetry protein-2 polynucleotide a polypeptide used to diagnose, treat and prevent autoimmune inflammatory responses -
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure
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AAB36529.
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 898 BP; 1376 A; 1140 C; 1162 G; 1220 T;
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    0 other;
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Qy QУ Qy Dр dd В QΥ В QУ Qy В Дb QУ В QΥ 멍 QΥ Query Ma Best Loo Matches 45 512 421 361 301 241 273 181 121 153 39  $^{3}$ 61 93 CCTTC TCAGC TGGAG AATTA AATTA. TCCCC TCCCC AAGTA AGTTT AGGCC. AGT AAGTA AGTTT AG-GG 11 S 498 GT TCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATCCCGGTCTCGGCGAA TGCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTCAGCTGTGACAACTC TACACCATCACCAAAACCCAGAATTTTATGATGAGAGTTAAAATAGAGTTGCCCAC 60 CCCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGTCTGCATGCGATGGA ATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGTCAGAAAACCGAATC AATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTAC AAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTTGGCTACTCCTGGCT ACGTGATGATCGCCT 500 CCCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGTCTGCATGCGATGGA AATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTAC AAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTTGGCTACTCCTGGCT Conservative 97.3%; Score 486.4; DB 21; Length 4898; 99.6%; Pred. No. 1.2e-152; ive 0; Mismatches 1; Indels 1; Gaps 480 420 452 332 180 120 152 360 392 300 240 272 212

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RESULT 12
AAC87975
ID AAC87975
XX
The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatori, hypotensive, antiinflammatory bowel disease classed activity of the transplantation rejection responses and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of THI1 cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e.g. arthritis, inflammatory bowel disease and increase and antended proliferation and other blood protein disorders. Disorders treated by disrupting CLASP-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension.
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29-OCT-1999;
13-DEC-1999;
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                                                                                                                                                                                                                                                           invention describes cadherin-like asymmetry protein-2
LASP-2 can have immunosuppressive, immunomodulatory,
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99US-0134114.
99US-0134117.
99US-0134118.
99US-0160860.
99US-0162498.
99US-0170453.
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2000US-0182296.
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immunodeficiency;
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                                               ASP-2; transmembrane protein; immune response; inflammatory; ke asymmetry protein; autoimmune disease; immunosuppressive; atory; antiinflammatory; antiarthritic; cytostatic; atory; antiinflammatory; antiarthritic; cytostatic; neuroprotective; antirheumatic; antianaemic; haemostatic; neuroprotective; ivity; transplantation rejection response; immunodeficiency; on; differentiation; inflammatory response; arthritis; y bowel disease; haematopoietic cell; blood protein disorder; irombocytopaenia; multiple sclerosis; rheumatoid arthritis; is; pregnancy induced hypertension; ss.
                                                                                                                                                                                                                                                                                                           CCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGTCTGCATGCGATGGA
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                                                                                                                                                    CLASP-2 nucleotide sequence #3.
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Pred. No. 1.2e-152;
0; Mismatches 1;
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Best Local
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99US-0134117.
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99US-0134117.

99US-0134118.

99US-0160860.

99US-0162498.

99US-0170453.

2000US-0176195.

2000US-0182296.
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The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an

hibit an immune response in a subject by a CLASP-2 protein to bind to another T cponse in a subject may also be inhibited hich specifically binds to CLASP-2. CLASF

inhibited by administering an SP-2. CLASP-2 polynucleotides,

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Matches
CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective; hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e,g, arthritis, inflammatory bowel disease and increase differentiation and proliferation of haematopoietic cells e.g. to treat anaemia, thrombocytopaenia and other blood protein disorders. Disorder: treated by disrupting CLASP-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension fine present sequence represents a preliminary CLASP-2 nucleotide sequence, from the present invention.
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                                                                                                                                                                                                         Isolated cadherin-like asymmetry protein-2 polynucleotide and polypeptide used to diagnose, treat and prevent autoimmune diseases and inflammatory responses -
                                                                                                                                                                                            Disclosure;
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99US-0162498.

99US-0170453.

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The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, cantiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, cantinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, antipolice, can be used to inhibit an immune response in a subject by interfering with the capture response in a subject by interfering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, can be used to prevent or treat a CLASP-2 proteins and antibodies can be used to prevent or treat a CLASP-2 mortains and antibodies can be used to prevent or treat a CLASP-2 mortains and cativity of THII cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory cresponse e,g, arthritis, inflammatory bowel disease and increase canemia, thrombocytopaenia and other blood protein disorders. Disorders treated by disrupting CLASP-2 function include multiple sclerosis, the present sequence represents a preliminary CLASP-2 nucleotide sequence, from the present invention.

Sequence 48 98 BP; 1376 A; 1140 C; 1162 G; 1220 T; 0 other;

QУ Qy DЬ Дb Qγ Query Ma Best Loc Matches 121 153 Loca £ 9 93 AAGTAA, AGTTTT AGTTTT TCAGCT TCAGCT 11 S 498 AGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTTGGCTACTCCTGGCT GCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTCAGCTGTGACAACTC ACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAAATAGAGTTGCCCAC 60 97.3%; Score 486.4; DB 21; Length 4898; ilarity 99.6%; Pred. No. 1.2e-152; Conservative 0; Mismatches 1; Indels 1; Gaps 180 212 120 152

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Вb	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Db	Qy
572 AGGCCACGTGATCGCCT 591	481 AGGCCACGTGATGATCGCCT 500	512 TGGAGCCCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGTCTGCATGCGATGGA 571	421 TGGAGCCCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGTCTGCATGCGATGGA 480	453 AG-GGATACTCAGGATCAGCATTTACATAATTTTTCCAGTACTGTCAGAAAACCGAATC 511	361 AGTGTATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGTCAGAAAACCGAATC 420	393 AATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTAC 452	301 AATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTAC 360	333 CCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGGCA	241 CCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGGCA	273 TCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATCCCGGTCTCGGCGAA 332	181 TCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATCCCGGTCTCGGCGAA 240

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## ALIGNMENTS

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US-08-936-165A-228/c
Sequence 228 Application US/08936165A
Patent No. 634852
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Howelto, Michael
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Michael
APPLICANT Michael
APPLICANTON DATA:
APPLICATION UNMBER: MICHAEl
APPLICATION DATA:
APPLICATION NUMBER: MICHAEl
APPLICATION MICHA
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APPLICANT: O'Mahony, Daniel J
APPLICANT: Cagney, Gerard
TITLE OF INVENTION: Composition and Method for Enha
TITLE OF INVENTION: Transport across Cell Layers
FILE REFERENCE: Docket No. 6346613: 98.1070.US
CURRENT APPLICATION NUMBER: US/09/160,496
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: US 60/059,644
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 6
                                                                                                                                            RESULT 3
US-08-961-083-203
                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                          ; ISSUE: 6
; PAGES: 1777-1788
; DATE: Dec 1993
; DATABASE ACCESSION NUMBER: D21837
US-09-160-496-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: 1; MOLECULE TYPE: US-08-936-165A-228
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US-09-160-496-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
TITLE: Occludin: A novel i
TITLE: at tight junctions
JOURNAL: J. Cell Biol.
VOLUME: 123
ISSUE: 6
                                                                                                  Sequence 203, Application US/0896108: Patent No. 6159469
GENERAL INFORMATION:
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Best Local
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APPLICANT: Choi et. & TITLE OF INVENTION: $
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Human Ge
STREET: 9410 Key We
CITY: Rockvill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Gallus
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                                                                                                                                                                                                         782
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Similarity 62.5%;
65; Conservative
                                                                                                                                                                                                                                                                                                                    Similarity 64; Conser
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nilarity 53.3%;
Conservative
                                               ADDRESS:
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Streptococcus
452
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Pred. No. 3.1;
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Mismatches
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US-08-961-527-81; Sequence 81, A
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Best I
                                                                                                                                                                                                                                                                                                                                          Patent No. 6420135
GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                               ZIP: 20850
COMPUTER READABLE FO
MEDIUM TYPE: Disk
COMPUTER: HP Vect
OPERATING SYSTEM:
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PRIOR APPLICATION DATA:
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MEDIUM
                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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TITLE OF INVENTION: St
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
            ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          104
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COUNTRY:
ZIP: 201
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                                       APPLICATION NUMBER: FILING DATE:
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                                                                                  CLASSIFICATION:
                                                                                                                                                                                                        COUNTRY: US ZIP: 20850
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 REGISTRATION NUMBER:
                                                                                                                                                                                                                                    STATE:
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62; Conserv
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                                                                                                                                                                                                                                             : 9410 Key West Avenue Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20850
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INVENTION: Streptococcus pneumoniae Polynucleotides
F SEQUENCES: 391
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: USA
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YPE: Diskette, 3.50 inch,

HP Vectra 486/33
                                                                                                                                                                                            EADABLE FORM:
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ilarity 53.9%;
Conservative
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HP Vectra 486
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                                                                                                                                                                  486,
                                                                                                            US/08/961,527
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36,373
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6/33
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RESULT 5
US-08-405-254-9/c
; Sequence 9, Application U
; Sequence 5773288
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     Query Match
Best Local S
Matches 90
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                                                                                                           ATTORNEY/ACE NAME: BENT, STELF...

REGISTRATION NUMBER: 29,, CREFERENCE/DOCKET NUMBER: 3322

REFERENCE/DOCKET NUMBER: 3322

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEPHONE: (202)672-5399

TELEFAX: (202)672-5399

TELEFAX: 322
                                                 08-405-254-9
                                                                                                                           TELEFAX: (202)6
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2520 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 16-MAR-19
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                             MOLECULE TYPE:
                                                                                                                                                                                                         FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9130
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TELECOMMUNICATION
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CITY: V
STATE:
                                                                      TOPOLOGY:
                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007
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 1 Similarity
90; Conserv
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62; Conser
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESS:
                                                                                                                                                                                                                     IMBER: US 0
17-JUN-1994
                                                                                                                                                                                                                                                                 MBER: US/08,
16-MAR-1995
                                                                                single
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M: PC-DOS/MS-DOS
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ROBERT
                                                          (genomic)
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ROBERT J.
PLANT GENES A
BIOSYNTHESIS
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53.9%;
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33229/299/PIHI
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              Score
Pred.
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Pred.
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  Mismatches
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11;
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  100;
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Db
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Best Local Sim
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                  TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   REFERENCE,
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AG
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE
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STRANDEDNE
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OPERATING
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CITY: 1
                                                                                                                                                                                                                                                                                            NAME: A. Anders Brookes REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I: Gil H. Choi
INVENTION: Enterococcus faecalis
SEQUENCES: 496
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9410 Key West Avenue
ckville
CCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGT 466
                                                                                              AATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTA 359
                                                                                                                                    ilarity
                                                                                                                                                                                                                                                                                   CATION INFORMATION:
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8043
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Conservative
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                                                                                                                      Score 29.4; D
Pred. No. 3;
0; Mismatches
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                                                                                                                                             Length 442;
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US-09-071-035-441
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US-08-924-747-15/c
; Sequence 15, Application
; Patent No. 6063570
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                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
GENERAL INFORMATION:
APPLICANT: MCGONIGLE,
APPLICANT: O'KEEFE, DA
TITLE OF INVENTION: SC
TITLE OF INVENTION: EN
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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MEDIUM TYPE: Diskette, 3.50 ir
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS versic
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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APPLICANT: Gil H. Choi
TITLE OF INVENTION: Ento
NUMBER OF SEQUENCES: 490
CORRESPONDENCE ADDRESS:
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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: 9410 Key
Rockville
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48.5%;
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DANIEL
SOYBEAN
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Pred. No. 3.6;
0; Mismatches
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No. 3.6;
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; ORGANISM: (
US-09-247-373B
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                                               SEQ ID NO 15
LENGTH: 1006
TYPE: DNA
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Best Local S
Matches 48
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Patent No
GENERAL 1
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SEQUENCE CH
LENGTH:
TYPE: nu
                                                                                              FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
                                                                                      SOFTWARE:
                                                                                                                                                                             APPLICANT:
TITLE OF INV
                                                                                                                                                                                                     APPLICANT:
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08-924-747-1
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
ORIGINAL SOURCE
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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TELEPHONE
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COMPUTER
MEDIUM
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TOPOLOGY:
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
IRRENT APPLICATION DATA:
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Match
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                                                                                                                                                                                                                         15,
61f
                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Similarity 60.8%; 48; Conservative
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DEDNESS: single
DGY: linear
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                       SOYBEAN
B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNICATION INFORMATION:
DNE: 302-892-8112
X: 302-773-0164
N FOR SEQ ID NO: 15:
CHARACTERISTICS:
1006 base pairs
                                                                                      3
                                                                                     G DATE: 1997-09-05
EQ ID NOS: 56
Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE:
                                                                                                                                                                                                                               Application US/09247373B.68954
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UNITED STATES
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                                                                                                                                                               MCGONIGLE, BRIAN
O'KEEFE, DANIEL
ENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
ICE: CL-1108-A
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INFORMATION FOR
                                                                                                                                                                                                                                                               NAME: FLOYD, LINDA AXAMETHY REGISTRATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: CL-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112 TELEFAX: 302-773-0164 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 1006 base pairs
                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE: TISSUE TYPE: S
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TITLE OF IN
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TOPOLOGY: linear
MOLECULE TYPE: cDN
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NAME: FLOYD, LINDA AXAME
REGISTRATION NUMBER: 33,
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STREET: 10
CITY: WILM
STATE: DEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MICROSOFT WORD SOFTWARE: MICROSOFT WORD VERSION
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-08-660-645A-1
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RATELECOMMUNICATION INFORMATION: TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 11:
                     APPLICANT:
APPLICANT:
APPLICANT
TITLE OF 1
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APPLICANT:
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COMPUTER
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION, NUMBER:
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CORRESPONDED
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CITY: 1
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RAL INFORMATION:
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PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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7152
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TE: 07-JUN-1996
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LICATION DATA:
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Tessier, Michel
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/ENTION: FERMENTATIVE CAROTENOID PRODUCTION
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Tessier, Michel
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Best Local S
Matches 82
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GENERAL INFORMATION:
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TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                               APPLICANT:
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COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PatentIn Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,
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CORRESPONDENCE ADDRESS:
                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                   TITLE OF INVENTION:
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ZIP: 07110
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CITY: 1
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REGISTRATION
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CIOR APPLICATION DATA:
APPLICATION NUMBER:
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ENTION: FERMENTATIVE
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APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION SEQUENCE C
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REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH. 706
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ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
RRENT APPLICATION DATA:
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GENERAL INFORMATION:
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION UNUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Search completed: February Job time: 888.628 secs
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Best Local Similarity 59.8%;
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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19, App	0 US-09-827-998-1	83	•	9.
Sequence 11, App	0 US-09-547-267-1	N	•	9.
equence 28, App	US-09-920-923-2	$\sim$	•	9.
1, Appl	US-10-126-912	82	٠	29.4
equence 7, Appl	US-10-126-912-	S		9
equence 2, Appli	US-10-126-912-2	45		9
ce 311, A	0 US-09-070-927A	92	•	9.
Séquence 1420, A	0 US-09-917-800A-14	70	•	9.
uence 37, App	US-10-114-893-37	89		9.
equence 3999, Ap	US-09-796-692-3999	$\mathbf{N}$	•	9.
Sequence 32600,	0 US-09-864-761-32	~	•	9.
e 9270,	US-09-796-692-927	$^{\circ}$	٠	9.

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RESULT 1

Sequence 1, Application US/09736969A

Patent No. US20020068302A1

GENERAL INFORMATION:

APPLICANT: Lu, Peter

APPLICANT: Carnan, Jonathan David
APPLICANT: Carnan, Jonathan David
APPLICANT: Carnan, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Candia III, Sipperial State
CURRENT FILING DATE: 020054-000411US
CURRENT FALING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-00-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR APPLICATION NUMBER: US 60/196,460
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,503
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RESULT 2
US-09-736-969A-7
; Sequence 7, Applicati
; Patent NO. US20020068
; GENERAL INFORMATION:
APPLICANT: Lu, Peter
; APPLICANT: Garman,
; APPLICANT: Candia 1
; APPLICANT: Arbor Vi
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                                                    APPLICANT: Lu, Peter
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: CLASP-4 Transmembrane Pr
FILE REFERENCE: 020054-000411US
CURRENT APPLICATION NUMBER: US/09/736,969A
CURRENT FILING DATE: 2000-12-13
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LOCATION: (95)..(6121)
OTHER INFORMATION: human
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APPLICATION NUMBER: UFILING DATE: 1999-10-APPLICATION NUMBER: UFILING DATE: 1999-10-
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PLICATION NUMBER: US 60/196,528
ING DATE: 2000-10-13
PLICATION NUMBER: US 60/240,503
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ATION NUMBER: US 09/547,276
DATE: 2000-04-11
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RESULT 3 US-09-736-9

Sequence 1, l Patent No. US

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Candia III, Albert Free
Carbor Vita Corporation
INVENTION: CLASP-5 Transme
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R APPLICATION NUMBER: US 60/196,267

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APPLICATION
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FILING DATE: 2000-12-1
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RESULT 6
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; Sequence 88, Application; Patent No. US20020120116; GENERAL INFORMATION:
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 6691 base pairs
                                                                                                                                                                                                                                                                                                                                                                        SEQUENC: 09-070-927A-8
                                                                                                                                  1776
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INFORMATION:
ANT: NAKAGAWA, SATOSHI
                                                                                                                                                            GCACGAAGA 140
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                                                                                                                                                                                                                     AAAAGCACCACCTGTTGCTCACATTCTTCCATGTCAGCTGACAACTCAAGTAAAGGAA 131
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                                                                                                                                GCAACAAGA
                                                                                                                                                                                                                                                                                                            ch 6.9%;
Similarity 54.3%;
70; Conservative
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APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
OR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human (
STREET: 9410 Key V
CITY: Rockville
STATE: Maryland
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E
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OF INVENTION: Enter
OF SEQUENCES: 982
                                                                                                                                                                                                                                                    CAAAAGAAATAGTCAAAGAACTAGATCAATATTGTTGGACAGCAAGCTGCCAA 1715
                                                                                                                                                                                                                                                                                                                                                                                                    YPE: nucleic acid TRANDEDNESS: double OPOLOGY: linear
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ER READABLE FORM:
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20020120116A1
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                                          Application US/09738626
). US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: SEQ ID NO: 88:
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                                                                                                                                   1784
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West Avenue
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Pred. No. 0.78;
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                         FILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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Best Local S
Matches 66
                SEQ
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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ORGANISM: Corynebacterium glutamicum
09-738-626-795
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    LENGTH:
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ID NO 795
ENGTH: 1314
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TATEISHI,
SENOH, AKI
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YOKOI, HARUHIKO
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ANDO, SEIKO
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SHI, NAOKO
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Pred.
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Mismatches
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LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (280373)..(280373)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (18397^
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US-09-771-208-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/771,208; CURRENT FILING DATE: 2001-01-26; PRIOR APPLICATION NUMBER: US 08/999,477; PRIOR FILING DATE: 1997-12-29; NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patent
SEQ ID NO 20
LENGTH: 659158
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (390986)..(391005)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
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Best Local
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TITLE OF INVENTION: CLONING OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCA
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54.1%;
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Pred. No. 91;
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RESULT 10
US-09-070-927A-394/c
; Sequence 394, Application |
; Patent No. US20020120116A1
; GENERAL INFORMATION:
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NAME/KEY: misc_feature
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US-09-771-208-20
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                                    ; SEQUENCE DESCRIPTION: US-09-070-927A-394
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SEQUENCE CHARACTERISTICS:
LENGTH: 14141 base F
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COMPUTER READABLE I
MEDIUM TYPE: I
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APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
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                                                                                                                                                                                                                  APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16 APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06 APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14
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5; Conservative
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)RMATION: n is unid
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CITY: Rockville
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                                                            STRANDEDNESS:
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REGISTRATION NUMBER:
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OF INVENTION: Enter
R OF SEQUENCES: 982
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RESULT 11
US-09-070-927A-1
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STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb statement of the state
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
ORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 4915 base pairs
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Patrick J.
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                                                                                                                                                                                                                        Similarity
56; Conserv
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APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
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STRANDEDNESS: double
TOPOLOGY: linear
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US-09-938-842A-3143/
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES
TITLE OF INVENTION: SAME, AND METHODS OF
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842&
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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Best Local S
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LENGTH: 2000
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                                                                                                                                                                             NUMBER OF SEQ I
SEQ ID NO 12649
LENGTH: 417
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ORGANISM: Arabidopsis t
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APPLICANT:
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                                                                                                                                  ORGANISM: Bos taur OTHER INFORMATION:
                                                                                                                                                               TYPE: DNA
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                            AAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTACAGTGTATACTCAGGATCAGCAT 382
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AAGAGATTCCCAATCATTCAAATCACAG
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                                                         6.2%;
Similarity 49.4%;
80; Conservative
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FION: Clone
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Pred. No. 5.1;
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RESULT 14
US-09-764-864-167
Sequence 1678,
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; TYPE: DNA
; ORGANISM: Homo s
US-09-764-864-1678
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Patent No.
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult |
NUMBER OF SEQ ID NOS: 1792
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                                                                                                                                     NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKli
     CURRENT
                                                                 COMPUTER
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                                                                                                                                                                                                                                                                                                                                                   228,
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1678
32191
COUNTRY: USA
ZIP: 19406-0939

4PUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%;
Similarity 58.1%;
64; Conservative
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US20020132753A1
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                                                                         STREET: 7
CITY: Kir
STATE: PA
COUNTRY:
ZIP: 1940
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Lonetto,
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Hodgson,
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Pratt, Julie
Reichard, Richard
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                                                                                                                                       SmithKline
                                                                                                                                                                                                                                                              Michael
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                                                                                                                                                                        No. US20020082234A1el Prokaryotic Polynucleotides Polypeptides and Their Uses
                                                                                                                                                                                                                                                                           David
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Pred. No. 40;
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APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/936,165
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 950549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERISTICS:
LENGTH: 1005 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-09-939-980-228
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Search completed: February Job time: 1286.29 secs
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Best Local Similarity 62.5%;
Matches 65; Conservative
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LOCUS
DEFINITION FEATURES source BE783911

ON 601470964F1 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:3874046 5',
mRNA sequence.

N BE783911

BE783911.1 GI:10205109

EST.

human.

SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 800)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LOnpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM9630 row: p column: 15

High quality sequence stop: 629. WA Library Preparation: Life Technologies, Inc.
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 465)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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/db_xref="taxon:9606"
/clone="IMAGE:3874046"
/clone=lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; S: Site_2: SalI; Cloned unidirectionally. Playerage insert size 1.75 kb. Library con Technologies."
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s sequence was derived from the FAPESP/LICR Human Cancer Genome
ject. This entry can be seen in the following URL
tp://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-TN0048-280
-001-g08&t3=2000-08-28&t4=1)
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/db_xref="taxon:9606"
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                                                               TCCCCTCCTGAAAGACGGAAGGG-TGGTGACAAGCGAGCACACATCCCGGTCTCGGCGA
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AAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTGGTTTCTA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7),
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 anda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 465)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-TN0048-280
800-001-e05&t3=2000-08-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 465.
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Shotgun sequencing of the human transcriptome
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TN0048"
/dev_stage="Adult"
/note="Organ: testis_normal; Vector: pucl8; Site_1: SmaI;
/note="Organ: testis_normal; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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               GTTTCTACAGTGTATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGTCAGAAA 412
                                                                   GGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACTCATCTG
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AGENCOURT_8858966 NCI_CGAP_Mam2 Mus m
IMAGE:6441934 5', mRNA sequence.
BQ919716
BQ919716.1 GI:22334414
EST.
house mouse.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM13965 row: o column: 23
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:6441934"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Satiste_2: NotI; Cloned unidirectionally. Primer: Oligo (Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

209 c 236 g 201 t 2 others
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1. 891
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                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itc,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuur,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                Computer-based methods for the mouse full-length cDNA construction of encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                      Please visit our web further details.
                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3526405E11"
/clone_lib="RIKEN full-L
/sex="male"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B"
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Mammalia; E
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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                                                                                                                                                          ; Metazoa; Chordata;
Eutheria; Rodentia;
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Pred. No. 3.8e-41;
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Sciurognathi; Muridae;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itc,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                               CAGCTGCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTCAGCTGTGACAACTCA
                                                                                                                                                                                         GTGCTACACCATTCTCAAAATCCAGATTTCTCTGATGAGGTGAAAATTGAACTACCAACA
                                                              CAACTCCATGGAAAACATCACCTTTTGTTCTCCTTTTACCACATCACATGTGACATCAAT
       AGTAAAGGAAGCACGAAGAAGAGGGGATGTCGTTGAAACCCCAAGTTGGCTACTCCTGGCTT
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
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Konno, H., Fukunishi, Y., Shibata, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (200), Please visit our web site (http://genome.gsc.riken.go.jp) for the mouse full-length cDNA construction and the construction of t
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/db_xref="taxon:10090"
/clone="G730050N08"
/clone_lib="RIKEN full-length enriched,
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Location/Qualifiers
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/cell_line="RCB-0558 LLC
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naka,T., Matsu
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Mammalia; E
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-NN0215-311000-007-b01&t3=2000-10-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 77.
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Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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+55-11-2707001
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                                                                                             D)
                                                                                                                                             /note="Organ: nervous_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization and subtraction: two approaches to discovery Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin "
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BF472403
BF472403.1 GI:11541586
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/organism="Mus musculus"
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/clone="UI-M-BH3-awc-c-08-0-UI"
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/clone="UI-M-BH3-awc-c-08-0-UI"
/clone="UI-M-BH3-awc-c-08-0-UI"
/clone="UI-M-BH3-M-S4 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hipoccampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.1,
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Tel: 81-45-503-9216

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNA
prepare full-length cDNA libraries for rapid discovery of n
prepare full-length cDNA libraries for rapid discovery of n
Thoue,K., Togawa,Y., Izawa,M., Ohara
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                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genome
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763030 TREN full-length enriched, B16
763030 RIKEN full-length enriched, B16
VA clone G370018M23 3', mRNA sequence.
763030 GI:16207943
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Rodentia;
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F10Y cells
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Ohara, E.,

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BASE CO
   ACCESSION VERSION KEYWORDS
                                                                                                               RESULT 10
BB222768
                                                                                                LOCUS
                                                                             DEFINITION
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Best Local Similarity 63.0
Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                            CTCCCTCCTAATTATTTAAGCATTCAAGATCCTAGCAAGTCCAAAGGCATGGTGGAAGTG
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,S., Kawai,J.,
Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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e mouse tissues
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/cell_type="B16 F10Y cells"
/note="pooled tissues; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"
137 c 101 g 141 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370018M23"
/clone_lib="RIKEN full-lo
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CDNA C
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63.0%;
                                                     345 bp mRNA linea:
N full-length enriched, adult male clone A530079G09 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 3e-3
O; Mismatches
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URL:http://genome.gsc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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RIKEN Mouse ESTs (Konno, H., et al.)
L Unpublished (2000)
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Mammalia; E
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mamm
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81-45-503-9222
81-45-503-9216
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                                                                               cap-trapper. cDNA went through one rounce to cap-trapper. cDNA went through one rounce 459.0. Second to Rot = 20.0 and subtraction to Rot = 459.0. Second to Rot = 20.0 and subtraction to Rot = 459.0. Second to Rot = 20.0 and subtraction to Rot = 459.0. Second to Rot = 459.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
/tissue_type="aorta and vein"
/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="A530079G09"
/clone_lib="RIKEN full-length enriched,
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Eutheria;
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/note="Site
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RIKEN Mouse ESTS (Konno, H., et al.)
Lupublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fig. 11. Contact: Yoshiki, A., Yoshima, Kanagawa 230-0045, Japan
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Tel: 01 ...
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile er trehalose and its application for the synthesis of full ler trehalose and its application for the synthesis of full ler or 
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
BB225426
BB225426
musculus
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/db_xref="taxon:10090"
/clone="A430083J17"
/clone_lib="RIKEN full-lerthymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/dev_stage="0 day neonate"
/lab_host="DH10B"
             285 bp mRNA linear RIKEN full-length enriched, adult male a cDNA clone A530092E21 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 10;
Pred. No. 2.8e-22;
); Mismatches 140;
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                                                                                                                   330
                              adult male aorta and vein
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GI:8894037

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REFERENCE
AUTHORS
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
Email: Genome-research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             details.
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rikel Genomic Sciences Center and Genome Science Laborator
                                                                                                                                                                                                                                                                                                                               contributed
                                                                                                                                                                                                                                                                                                                                                           RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="aorta
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
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/clone__lib="RIKEN f
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Division of Experimental Animal Research in Ril
buted to prepare mouse tissues. 1st strand cDNA
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

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Automated filtration-based high-throughput plasmid preparation
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                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Contact: Yoshihide Hayashizaki
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
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Mus musculus
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/db_xref="taxon:10090"
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hypothalamus"
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RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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URL:http://genome.gsc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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RIKEN Mouse ESTS (Konno, H., et al.)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                          System. Genome Res
Carninci, P. and I
High-efficiency:
19-44 (1999)
                                                                                                              Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

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Thermostabilization and thermoactivation of thermolabile e trehalose and its application for the synthesis of full le cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., K Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,Y. and Hayashizaki,Y.
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/clone="E130012K13"
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Title:
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Tashi

ro, H., Yamazaki, M., Watanabe, K., Kumagai, A.,

Itakura,S.,

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## SUMMARIES

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L Unpublished
E 2 (bases 1 to 2469)
S Isogai, T. and Yamamoto, J.
Direct Submission
AL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB.
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Macaca fascicularis adult male brain pactone_lib:macaque brain cDNA library Qr

Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhir
Cercopithecinae; Macaca.
                                                                                                                                                                                                                     1 Similarity 96.
485; Conservative
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libraries
Unpublished
2 (bases 1
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Osada, N.,
Terao, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2516)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (11-OCT-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
Lab host: TOP10
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                                                                                                                                                                                                                                                                                                                                                               657
                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="hypothetical protein"
/product="hypot
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/tissue_type="brain parietal lobe/clone_lib="macaque brain cDNA li/dev_stage="adult"
1242. .>2516
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                                                                                                                                                                                                                                               94.9%;
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                   Score 475.4; DB 9; Pred. No. 6.6e-116; ); Mismatches 16;
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brain cDNA lib
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Sequence 7
AX255048
AX255048.1
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7506)
Rastelli, L.K. and Gerritsen, M.
Angiogenesis-associated proteins, and nucleic acids encoding the
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ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGA
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larity 99.8%;
Conservative (
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Corporation (US); GENENTECH,
Location/Qualifiers
1. .7506
                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
1689 c 1764 g 190
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AUTHORS
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Schwartz, M.A.
Zizimin1, a novel Cdc42 activator, revea
exchange-exchange factor domain for rho
Nat. Cell Biol. (2002) In press
2 (bases 1 to 7522)
Meller, N. and Schwartz, M.A.
Direct Submission
Submitted (05-JUL-2002) Cell Biology, The
Institute, 10550 N. Torrey Pines Rd., La
Location/Qualifiers
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 7522)
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EEAQSLFVTECIKTYNSDWHLVNYKYEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVD
KDEDAASLGSQKGGITKHGWLYKGNMNSAISVTMRSFKRRFFHLIQLGDGSYNLNFYK
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NKILQLNFEAAMQEKRNGDSHEDDEQSKLEGSGGGLDSYLPELAKSAREAEIKLKSES
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LHEAAMQYPKQGIFSVTCPHPDIFLVARIEKVLQGSITHCAEPYMKSSDSKVAQKVL
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FVPGIPKHTQPYTIVNHLYVYPKYLKYDSQKSFAKARNIAICIEFKDSGYLKSIDMLKLL
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SKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHIPVSANLPSGYLGYQELGMGRHYG
PEIKWVDGGKPLLKISTHLVSTVYTQDOHLHNFFOYCQKTESGAQALGNELVKYLKSL
PEIKWVDGGKPLLKISTHLVSTVYTQDOHLHNFFOYCQKTESGAQALGNELVKYLKSL
HAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVIIHVVAQCHEEGLESHLRSY
VKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFTISNKLLKYSWFFFDVLIKSMA
QHLIENSKVKLLRNQRFPASYHAVETVVNMLMPHITQKFRDNPEASKNANHSLAVFI
KRCFTFMDRGFYFKQINNYISCFAPGGDPKTLFEYKFEFLRVVCNHEHYIPLNLPMPFG
KGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLIAISVLKNLLIK
HSFDDRYASRSHQARIATLLLPLFGLLLENVQRINVRDVSPFPVNAGMTVKDESLALP
AVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSG
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56. .6265
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activator"
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/product="zizi
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                                                                                                                                                                                       GAACGACCCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAC
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ACGGAAAG
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27; Conservative
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TYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARTGMMHARLQQLGSLDNSLTFNHS
YGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVY
LCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCYEILKCCNSKLSSIR
TEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLIAFKNQLLADHGHNPLMKKVFDVY
CANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQYSLAKSYAST
PELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRKEAVQWEPPLLPHSHSA
CLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNEDVLMELLEQCADGLW
KAERYELIADIYKLIIPIYEKRRDFERLAHLYDTLHRAYSKVTEVMHSGRRLLGTYFR
VAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGS
ENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEM
PFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKK
VAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKRYPDNKVKLL
KEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQLG"
46 a 1694 c 1774 g 1908 t
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Pred. No. 8.1e-103;
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AB028981
                                                                                REFERENCE
AUTHORS
                                                                                                                                                                              SOURCE
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                                                                                                                                              ORGANISM
  JOURNAL
                                                   TITLE
                                                                                                                clone:hhl2146s1.
Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                               Kikuno,R.,
Tanaka,A.,
                                                                                                                                                                                                                          AB028981 7545 bp
Homo sapiens mRNA for KIAA1058 p
AB028981 -- CALLERY
                                                                                                                                                                              Hom
                                                                                                                                                                                                              AB0
                                 Pre
                                                                                                               Mammalia;
kuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N., naka,A., Kotani,H., Nomura,N. and Ohara,O. ediction of the coding sequences of unidentified human genes V. The complete sequences of 100 new cDNA clones from brain de for large proteins in vitro A Res. 6 (3), 197-205 (1999)
                                                                                                                                                                                                               28981.2
                                                                                                                                                                             sapiens brain cDNA to mRNA, clone_lib:pBluescriptII
                                                                                                                                                                                                                 GI:20521745
                                                                                                                   Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae
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protein,
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Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:5689452.
                                                                                                                                            2175
                                                                                                                                                       /Godon_Start=1
//godon_Start=1
//product="KIAA1058"
//product="KIAA1058 protein"
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/db_xref="taxon:9606"
/chromosome="13"
/clone="hh12146s1"
/tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained bysubcloning of the fragments derived from two cDNA clones (1 - 1846 was derived from ef00877 and 1847 - 7545 was derived from hh12146)."
1. .7545
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                                                                                                                                                 Gene Collection (MGC), Institute, 31 Center DUSA
NIH-MGC Project URL: h Contact: MGC help desk Email: cgapbs-r@mail.n Fissue Procurement: Jechna Library PreparaticDNA Library Arrayed bDNA Sequencing by: Bay Sequencing Center Code: BCM-HGSC Web site: http://www.h
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Direc
Submi
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BC009
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: i Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC009134 2998 bp mRNA linear ROD 07-AUG-2002 Mus musculus, Similar to hypothetical protein FLJ20220, clone MGC:11827 IMAGE:3596515, mRNA, complete cds.
                                                                                                         Gunar,
Yoon,
                                                                                          Richa
                                                                                                                                         Conta
                                                                                        Intact: MGC help desk

Mail: cgapbs-r@mail.nih.gov

Ssue Procurement: Jeffrey Green M.D.

NA Library Preparation: Life Technologies, Inc.

NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Requencing by: Baylor College of Medicine Human Genome squencing Center

Inter code: BCM-HGSC

In site: http://www.hgsc.bcm.tmc.edu/cdna/

Intact: amg@bcm.tmc.edu

Inaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S., Son, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, Chards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                        tted (05-JUN-2001) National Institutes of Health, Mammalian Collection (MGC), Cancer Genomics Office, National Cancer tute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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134.1 GI:14318664
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                                                                                                          Hulyk, S.W., Hale, S
Martin, R.G., Muzny,
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y, D.M.
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Euteleostomi;

Murinae;

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Best Local Similarity 88.2%;
Matches 398; Conservative
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                                                                                                                                                  CTGATGTGAAGGACTTAACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGA
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                                                                                                                                                                                                           AGGAGCATGAGAACGACCCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCT
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X68101
X68101.1 GI:
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Rattus norveg
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/product="Similar to hypothetical protein FLJ20220"
/product="Similar to hypothetical protein FLJ20220"
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LGTYFRVAFFGQGFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQD
SGKVNPKDLDSKFAYIQVTHVTPFFDEKELQERRTEFERCHNIRRFMFEMPFTQTGKR
QGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLC
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EACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSDIMREQICPLEEKTSVLPNSL
HIFNAISGTPTSTVVQGLTSSSSVV"
85 a 655 c 768 g 740 t
   norvegicus
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/clone="MGC:11827 IMAGE:3596515"
/tissue_type="Mammary tumor. C3(
ductal carcinoma. 5 month old vi
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
381. .1634
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1. .2998
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/db_xref="taxon:10090"
                                550419
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Rattus.
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Pianese, L.
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iciello,A., Monticelli,A., Musti,A.M.,
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ologia Cellulare e Molecolare, Via Pansini, Naples, ITALY
(bases 1 to 3227)
                                                                                                                                                                                                                                          CGCAGACGTGGTTGGCATTGGAGGAACCAGATTCCAGCAGTCCTTGTCTATCATC
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LMATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMC
YVHVTALVAEYLTRKEADLALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPNI
DEEASMMEDVGMQDVHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSPSMKSGG
TLETTHLYDTLHRPYSKVTEVITRAAGSWDLLPGGLFGQGFFEDEDGKEYIYKEPKLT
-PLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFAYIQVTHVTPFFDEKELQ
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AFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYRE
IRKELSDIIVPRICPGEDKRATKFPAHLQRHQRDTNKHSGSRVDQFILSCVTLPHEPH .
VGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGKVHIFF"
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Location/Qualifiers
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<1. .2218
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/cell_line="FRTL-"
/clone_lib="lambdaGT"
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/strain="Fischer"
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Best Local Similarity 71.8%;
Matches 359; Conservative
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                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 2610)
Yue, H., Tang, Y.T., Hillman, J.L., Lal, P., I
Azimzai, Y., Yang, J., Reddy, R. and Lu, D.A.
Human intracellular signaling molecules
Patent: WO 0077040-A 62 21-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                   CGAAAAAATTATTTCCTAACGGATGTTCAGCGTTCAAGAAATTACTCCCAATATAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          AATAATTTTGCAAATAGTGACAGACCTATGAAGGCAACTGCCTTTCCCGCAGAAGTCAAA
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/db_xref="taxon:9606"
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d Lu,D.A.
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S Isogai, T., Otsuki, T. and Sugiyama, 1.

Direct Submission

L Submitted (24-oCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, and Biotechnology Center, National Institute of Technology and
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E 1

S Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project
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KQGCIEEQCKRRTILTTŠNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELQKL
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Lu,P., Garman,J.D. and Candia,A.F. Clasp-4 transmembrane protein Patent: WO 0142294-A 1 14-JUN-2001; Arbor Vita Corporation (US)
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VKELSDIHHGILGELGDTMHSPMSNTLHVFCAISGTSSDRGYGSPRYAEV"

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QУ Qy QΥ Вр В Дb Вþ Qy δÃ QУ QУ Вр QΥ VΩ dd Дb B Query Mate Best Local Matches 4502 4742 4682 4622 4 182 562 122 442 862 302 242 422 802 362 62 Match Local Sir es 359;  $\sim$ GACTT CTGATA GACTT AACGA( TATAC CCAGA AATAA CGAAA CGGAA TTTTC. CTCTC CCCGAGCTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGAT AACAA CTGAT TACACTGGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAG 61 GAGGA AAAGA imilarity 71.0
; Conservative AGAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACA AACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAG AAAATTATTTCCTAACGGATGTTCAGCGTTCAAGAAAATTACTCCCAATATAGAT AGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATCGAC GCTCAGGAAAACCTGGCTTGATAGCATGGCCAAGATTCATGTAAAAAATGGAGAT CCCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACG AGCTGATGTAGCACTAAGCGGAGGATCAAGATTTCAGGAGTCTTATTCATTATC AGCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATC 121 CAAAAGGAAAACCTTTTTGAGGACACATCTACAGATAATAATTGCTGTAAGCCAA GGCCTCCATGATGGA CCTGAAATGCTAATTGATCTCCAGTATAGCTTAGCCAAGTCCTATGCAAGCACC 54.1 71. % % 80 % 501 0; Score 274.4; DB 6; Pred. No. 2.6e-62; ); Mismatches 141; Length 6454; Indels 0; Gaps 421 4621 4501 4861 4681 181 4921 481 361 4741 301 241 4561

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Best Local Similarity 71.2%;
Matches 356; Conservative
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Clasp-4 transmembrane protein
Patent: WO 0142294-A 99 14-JUN-2001;
Arbor Vita Corporation (US)
Location/Qualifiers
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P., Garman, J.D. and Candia, A.
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/db_xref="taxon:32630"
/note="polynucleotide fragment"
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Patent: WO 0142294-A 7 14-JUN-2001;
Arbor Vita Corporation (US)
Location/Qualifiers
                                       CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGAT
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SRNVNYSLASFLKCCLTLMDRGFVFNLINDYISGFSPKDPKVLAEYKFEFLQTICNHE

HYIPLNLPMAFAKPKLQRVQDSNLEYSLSDEYCKHHFLVGLLLETSIALQDNYEIRY

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PNSASRDEFPCGFTSPANRGSLSTDKDTAYGSFQNGHGIKREDSRGSLIPEGATGFPD

QGNTGENTRQSSTRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWNKVSPQE

LINILILLEVCLFHFRYMGKRNIARVHDAWLSKHFGIDRKSQTMPALRNRSGVMQARL

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TTSNSFPYVKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSSTDVDMIQUQLKL

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/db_xref="taxon:9606"
/note="human CLASP-4 cDNA"
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Clasp-4 transmembrane protein
Patent: WO 0142294-A 97 14-JUN-2001;
Arbor Vita Corporation (US)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="polynucleotide fragment"
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Direct Submission

L Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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jiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
ii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
shikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
cine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K.,
nehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A.,
vakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.,
l Isogai,T.

O human cDNA sequencing project
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Preliminary CLASP-	8797	21	38	00.	501	10	

## ALIGNMENTS

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Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome; blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation; CLASP; gene; ss.
(ARBO-)
(GARM/)
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ARBOR VITA CORP.
GARMAN J D.
CANDIA A F.
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Best Local Similarity 100.0%;
Matches 501; Conservative
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)B; ABG61673.
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                                                                                                                                                                                                                                                                                                                     Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome; blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation;
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GARMAN J D.
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The invention relates to an isolated polypeptide (I) comprising a acid sequence that has 90 % sequence identity to one of the human cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, sequences (PS). (I) is useful for identifying a compound or agent

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detecting a cLASP-2 polypeptide. An antibody (II) is useful for classed and cLASP-2 polypeptide in a sample. (II) is useful for thibiting a immune response in a subject. A pharmaceutical composition comprising a nucleic acid encoding (I), or (II) is useful for preventing comprising a nucleic acid encoding (I), or (II) is useful for preventing cor treating a CLASP-2 mediated disease e.g. an autoimmune disease, where cor fill cells. CLASP-2 polynucleotides are useful as probes or primers for classed the autoimmune disease is caused or exacerbated by increased activity of the control of the classed activity of the cells and construct transgenic and knockout animals, e.g., for screening of cLASP-2 agonists and antagonists. CLASP-2 polypeptides or polynucleotides can construct transgenic and knockout animals, classed activation, differentiation of immune cells and can treat or detect deficiencies of disorders of haematopoietic cells. CLASP-2 polypeptides or classed activation and proliferation of immune cells and can treat or detect disorders associated with a decrease in certain (or many) types of haematopoietic cells, including the pluripotent stem cells to treat those classed activation and protein disorders (e.g., agammaglobulinaemia, variable classed, multiple sclerosis, rhoumatoid arthritis, lupus, and inclassed constructions of properties of the invention. Abdison's disease, haemolytic anaemia, or classed disease, can be used to treat anaphlaxis or creat can be used to treat anaphlaxis or ca
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Mismatches 0;
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an immune arthritis, New human cadherin-like asymmetry protein(s) (CLASP)-2 for modulating cesponse, and for treating multiple sclerosis, rheumatoid endometriosis, lupus, autoimmune thyroiditis, septic shock

Disclosure Figure 1; 245pp; English.

of TH1 cells. CLASP-2 polynucleotides are useful as probes or primers for cribozyme-mediated inhibition), for gene knockout, etc. The CLASP-2 cantibodies or are used as therapeutic polynucleotides can express CLASP-2 polypeptides, produce anti- CLASP-2 cantibodies or are used as therapeutic polypeptides. The CLASP-2 colynucleotide or fragments can be used in diagnostics (e.g., as probes cfor CLASP-2 expression), as a lymphocyte marker and for therapeutic purposes. CLASP-2 polynucleotides can express class-2 polypeptides. The CLASP-2 colynucleotides can screening of CLASP-2 agonists and antagonists. CLASP-2 colynucleotides can screening of CLASP-2 agonists and antagonists. CLASP-2 colynucleotides or polynucleotides can treat deficiencies or clasp-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 polypeptides or polynucleotides can treat deficiencies or clasp-2 polypeptides or polynucleotides can treat or detect deficiencies or disorders of the immune cystem, by activating or inhibiting the croplynucleotides can increase differentiation and proliferation of haematopoietic cells, including the pluripotent stem cells to treat those clasorders associated with a decrease in certain (or many) types of haematopoietic cells e.g., immunologic deficiency syndromes including blood protein disorders (e.g., agammaglobulinaemia, or haemoglobulinaemia, ataxia telangiectasia, common variable commondeficiency, Digeorge syndrome, lymphopenia, thrombocytopenia, or haemoglobulinaemia, claspes, e.g., Addison's disease, haemolytic anaemia, crave's disease, multiple sclerosis, rheumatoid arthritis, lupus, candometriosis, autoimmune thvroiditis, and antoimmune nulmonarv Grave's dis endometrios inflammatio hypersensit The invention relates to an isolated polypeptide (I) comprising an amino acid sequence that has 90 % sequence identity to one of the human cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2A, 2B, 2C, 2E) sequences (PS). (I) is useful for identifying a compound or agent that binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for detecting a CLASP-2 polypeptide in a sample. (II) is useful for inhibiting a immune response in a subject. A pharmaceutical composition comprising a nucleic acid encoding (I), or (II) is useful for preventing or treating a CLASP-2 mediated disease e.g. an autoimmune disease, where the autoimmune disease is caused or exacerbated by increased activity tivity to an antigenic molecules, organ rejection or t disease (GVHD) and inflammation. ABK84922-ABK85018 , autoimmune thyroiditis, and autoimmune pulmonary CLASP-2 can be used to treat anaphylaxis or graft-

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AGCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCAT

2559

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AGCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCAT

Db

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GGACTTAACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGA

CAACAACTGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAA

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240

CTGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAA

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GAACGAC |||||||| GAACGAC

GCCCGAGCTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGA

360

300

CCCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAC

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CC (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, contains and contains and neuroprotective activities. CLASP-2 can be contained in thibit an immune response in a subject by interfering with the containing of a CLASP-2 protein to bind to another T cell or B cell. An containing the containing and antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, contained disease, such as an autoimmune disease caused or exacerbated contained disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and cugment immune responsiveness in immunodeficiency states, inhibit colliferation and differentiation of cells involved in an inflammatory contained by disrupting clasp-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence encodes human CLASP-2, which is used in the ceremplification of the present invention.
                           Qy
                                                      Query Ma
Best Loo
Matches
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
13-DEC-1999;
14-JAN-2000;
14-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated cadherin-like asymmetry protein-2 polynucleotide apolypeptide used to diagnose, treat and prevent autoimmune inflammatory responses -
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P-PSDB; AAB
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                                                       Conservative
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99US-0134114.

99US-0134117.

99US-0134118.

99US-0160860.

99US-0162498.

99US-0170453.

2000US-0176195.

2000US-0182296.
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                                                                  100.0%;
                                                                                                            1117 C;
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                                                    Score 501; DB 21;
Pred. No. 1.1e-141;
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                                                                                                            1136 G;
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The present invent (CLASP-2). CLASP-2 antiinflammatory, antianaemic, haemoused to inhibit an ability of a CLASP
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
13-DEC-1999;
14-JAN-2000;
14-FEB-2000;
                                                                                            Isolated cadh polypeptide u inflammatory
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P-PSDB; AAB36528.
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                                         sent invention (2). CLASP-2 can
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  CLASP-
                      haemostatic
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99US-0134114.

99US-0134117.

99US-0160860.

99US-0162498.

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tion describes cadherin-like asymmetry protein-2

2 can have immunosuppressive, immunomodulatory,
antiarthritic, cytostatic, hypotensive, antirheumatic,
ostatic and neuroprotective activities. CLASP-2 can be
n immune response in a subject by interfering with the
P-2 protein to bind to another T cell or B cell. An
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                                                       cadherin-like asymmetry protein
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blood prot ataxia tel thrombocyt

oimmune disease; haematopoietic disorder; Digeorge syndrome; ein disorder; agammaglobulinaemia; dysgammaglobulinaemia; angiectasia; common variable immunodeficiency; lymphopenia; openia; haemoglobinuria; Addison's disease; Grave's disease;

Human;

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caunerin-like asymmetry protein(s) (CLASP-24, 28, 26, 28)

c sequences (PS). (I) is useful for identifying a compound or agent that binds CLASP-2 polypeptide in a sample. (II) to (I) is useful for identifying a compound or agent that compound or agent that the compound of the composition or inhibition and insert the autoimmune disease is caused or exacerbated by increased activity of the autoimmune disease is caused or exacerbated by increased activity of the autoimmune disease is caused or exacerbated by increased activity of the autoimmune disease is caused or exacerbated by increased activity of the autoimmune disease e.g. an autoimmune disease, where the autoimmune disease e.g. an autoimmune disease or ribozyme-mediated inhibition), for gene knockout, etc. The CLASP-2 polymucleotides can expression (e.g., antisease articipally etc. The CLASP-2 polymucleotides can construct transgenic and knockout antimals, e.g., for screening of CLASP-2 polypeptides. The CLASP-2 polymucleotides can construct transgenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polymucleotides can treat deficiencies or disorders of the immune cells and can treat or detect deficiencies or disorders of haematopoietic cells and can treat or detect deficiency. Dispersion of immune cells and can treat or detect automatic cells, including the pluripotent stem cells to treat those haematopoietic cells, including the pluripotent stem cells to treat those disorders associated with a decrease in certain (or many) types of haematopoietic cells, including the pluripotent stem cells to treat those haematopoietic deficiency, Dispersion or treat to cells and can be de
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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hypersensitivity to an antigenic molecules, organ rejection or versus-host disease (GVHD) and inflammation. ABK84922-ABK85018 represent cadherin-like asymmetry protein (CLASP) coding seque
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                                                                                                                      Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome; blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation;
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CC acid sequence that has 90 % sequence identity to one of the human CC cadherin-like asymmetry protein(s) (CLASP) 2 (hCLASP-2A, 2B, 2C, 2E) CC detecting a CLASP-2 polypeptide. An antibody (II) to (I) is useful for comprising a cumpound or agent that CC binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for comprising a nucleic acid encoding (I), or (II) is useful for comprising a nucleic acid encoding (I), or (II) is useful for preventing corrections or inhibiting a immune classes is caused or exacerbated by increased activaty corrections or inhibition), for gene knockout, etc. The CLASP-2 polynucleotides are useful as probes or primers for complynucleotides can express CLASP-2 polynucleotides. The CLASP-2 coplynucleotides or are used as therapeutic polypeptides. The CLASP-2 coplynucleotide or fragments can be used in diagnostics (e.g., as probes coplynucleotide or fragments can be used in diagnostics (e.g., as probes coplynucleotides can screening of CLASP-2 agonists and antagonists. CLASP-2 polynucleotides can construct transgenic and knockout composed to the immune system, by activating or inhibiting the collisorders of the immune system, by activating or inhibiting the collisorders of the immune system, by activating or inhibiting the collisorders associated with a decrease in certain (or many) types of compositic cells, including the pluripotent stem cells to creat those construct collisors or disorders of haematopoletic cells clasp-2, immunologic deficiency syndromes including the pluripotent stem cells to creat those industrial telanguic tasian (or many) types of communodeficiency, Digeorge syndrome, lymphopenia, thrombocytopenia, or immunodeficiens, Digeorge syndrome, lymphopenia, thrombocytopenia, or immunodeficiens, Digeorge syndrome, lymphopenia, thrombocytopenia, or
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14-JAN-2000
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99US-0134114.

99US-0134117.

99US-0134118.

99US-0160860.

99US-0162498.

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Isolated cadherin-like asymmetry protein-2 polynucleotide polypeptide used to diagnose, treat and prevent autoimmune inflammatory responses -

autoimmune

diseases

and

and

Fig

10A;

286pp;

English.

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RESULT 10
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ID AAC87975
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AC AAC87075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 501; Conservative 0
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                                                                               standard;
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Pred. No. 1.1e-1
); Mismatches
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-141;
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180

2770

240

480

Query Match
Best Local Simi
Matches 501;

Conservative

<u>,</u>

Mismatches

Indels

0,

Gaps

0,

100.0%;

Score 501; DB 21; Pred. No. 1.1e-141;

Length 4898;

Sequence

48

86

вP;

1376 A;

1140 C;

1162 G;

1220 T;

0

other;

420

360

300

2830

2890

120

2650

60

0;

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CC (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antianthritic, cytostatic, hypotensive, antirheumatic, cu antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be considered to inhibit an immune response in a subject by interfering with the ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an contibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, considered disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e.g., arthritis, inflammatory bowel disease and increase treated by disrupting CLASP-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence represents a preliminary CLASP-2 nucleotide sequence, from the present invention.
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
13-DEC-1999;
14-JAN-2000;
14-FEB-2000;
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inflammatory
anaemia; thr
endometriosi
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immunomodula
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99US-0134114.
99US-0134117.
99US-0134118.
99US-0160860.
99US-0162498.
99US-0170453.
2000US-0176195.
                                                                                                                                                                                                                                                                                                                                              invention describes cadherin-like asymmetry protein-2
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
13-DEC-1999;
14-JAN-2000;
                                                                                                                                                                        CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective; hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis; endometriosis; pregnancy induced hypertension; ss.
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 99US-0129171.

99US-0134114.

99US-0134117.

99US-0134118.

99US-0160860.

99US-0162498.

99US-0170453.

2000US-0176195.
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Sequence

48

98 BP; 1376 A; 1140 C; 1162 G; 1220 T;

0 other;

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antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of THII cells. They can also be used to treat chypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory crasponse e.g., arthritis, inflammatory bowel disease and increase differentiation and proliferation of haematopoietic cells e.g. to treat chipe the discussion of the multiple sclerosis, treated by disrupting CLASP-2 function include multiple sclerosis, theumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence represents a preliminary CLASP-2 nucleotide sequence, from the present invention.
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QУ Dр Db δÃ Dφ Дb VΩ QУ QУ B QУ QУ Вb Qy Вb Query Ma Best Loo Matches 25 2891 2771 2711 28 241 181 121 651 301 951 361 y Match Local S 91 61 31 GAACG! GGACTTAACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGA GCTGATAGCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCAT 120 TCTCT 11111 AC I TCTCT GCCCG GAACG ACG σH Si 01; GA |-GA. imilarity AAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATCGA 480 AGCTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGA ACCCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAC CAGAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCAC CAGAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCAC 100.0%; larity 100.0%; Conservative 0, 0; Score 501; DB 21; Pred. No. 1.1e-141; Mismatches 0; Length 4898; Indels 0 Gaps 2770 2650 2830 2950 2890 3010 360 300 240 0

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RESULT 12
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    (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, cused to inhibit an immune response in a subject by interfering with the classific antibody which specifically binds to cLASP-2. CLASP-2 polynucleotides, con be inhibited by administering an immune response in a subject may also be inhibited by administering an classific antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, concentrated disease, such as an autoimmune disease caused or exacerbated concentration and antibodies can be used to prevent or treat a CLASP-2 polynucleotides, concentrated disease and activity of TH11 cells. They can also be used to treat classed activities, prevent transplantation rejection responses and congment immune responsiveness in immunodeficiency states, inhibit confideration and differentiation of cells involved in an inflammatory concentration and proliferation of haematopoietic cells e.g. to treat consemia, thromboovtonsenia and other consenia.
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14-MAY-1999;
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99US-0134114.

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                                                          ASP-2; transmembrane protein; immune response; inflammatory; letery; antiinflammatory; antiarthritic; cytostatic; latory; antiinflammatory; antiarthritic; cytostatic; latory; antirheumatic; antianaemic; haemostatic; neuroprotective; invity; transplantation rejection response; immunodeficiency; lon; differentiation; inflammatory response; arthritis; ry bowel disease; haematopoietic cell; blood protein disorder; irombocytopaenia; multiple sclerosis; rheumatoid arthritis; is; pregnancy induced hypertension; ss.
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The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the ability of a CLASP-2 protein to bind to another T cell or B cell. An

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GTCATTACCCCAAACATCGA 3070	11 ACGGAAAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATCGA	3011	Db
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• Search completed: February 7, 2003, 07:08:07 Job time: 158.085 secs

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US-09-205-426-169
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PCT-US94-01101-1
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ALIGNMENTS

## Sequence 14, Application Patent No. 6355451 GENERAL INFORMATION: CORN\_ ADDR\_ STREET: 22. CITY: Boston STATE: MA COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2./ TURRENT APPLICATION NUMBER: US/08/979,608A TATE: 26-No. 6355451-1997 TATE: 26-No. 6355451-1997 TATA: US 60/048,547 CORKENT APPLICATION NUMBER: US/08/979,608A FILING DATE: 26-No. 6355451-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/048,547 FILING DATE: 03-JUN-1997 APPLICATION NUMBER: US 60/031,930 FILING DATE: 27-NOV-1996 ATTORNEY/AGENT INFORMATION: NAME: Myers, Louis REGISTRATION NUMBER: 35,965 REFERENCE/DOCKET NUMBER: 10797-002001 TELEPHONE: 617/542-5070 TELEPHONE: 617/542-8906 FORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 4722 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear FEATURE: NAME/KEY: LOCATION: TOTENCE DESCRI NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & 1 STREET: 225 Frankl $_{\rm F}$ Application US/08979608A 55451 Lees, Robert ... Law, Simon W. Arjona, Anibal A. INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS - CFOHENCES: 42 E/KEY: Coding Sequence ATION: 61...1731 DESCRIPTION: SEQ ID NO. Ann M NO: 14: 10797-002001 (formerly 3983/59818) 2.0

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REFERENCE/DOCKET NUMBER: 2815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US
FILING DATE: July 13,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/8
FILING DATE: March 23, 1
ATTORNEY/AGENT INFORMATION:
NAME: Ramon A. Klitzke I
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                     TYPE:
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IBM PC compatible
SYSTEM: MS DOS
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                                                                                                    Genomic
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GENES AND ENZYMES INVOLVED
THE MICROBIAL DEGRADATION OPENTACHLOROPHENOL
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rade Center
lmon Street
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23, 1992
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3, 1992
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US-08-276-887A-
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Best Local S
Matches 107
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Patent No. 5512-1.
Pareral INFORMATION:
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                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/914,282
FILING DATE: July 13, 1992
APPLICATION NUMBER: 07/856,015
FILING DATE: March 23, 1992
FILING DATE: March 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Ramon A. Klitzke II
                                                                                                                              INFORMATION
SEQUENCE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER RE MEDIUM TY COMPUTER:
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       MOLECULE TO
DESCRIPTO
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 5.1/PC Gene CURRENT APPLICATION DATA:
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COUNTRY:
ZIP: 972
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STREET:
STREET:
                                                                 TYPE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US FILING DATE: July 18, CLASSIFICATION: 435
                                                                                                                                                                                                         NAME: Ramon A. Klitzke II
REGISTRATION NUMBER: 30,188
REFERENCE/DOCKET NUMBER: 28
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
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CLASSIFICATION:
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                                                TOPOLOGY
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                                                                                                                         HONE: (503) 226-7391

AX: (503) 228-9446

ON FOR SEQ ID NO: 3:

E CHARACTERISTICS:
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TYPE: Di
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                                                                                      Nucleic Acid
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One World Trade Center
121 S.W. Salmon Street
Suite 1600
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Cindy S. and Xun, Luying
GENES AND ENZYMES INVOLVED
IN THE MICROBIAL
DEGRADATION OF

PENTACHLOROPHENOL

IBM PC compatible

MS DOS

US/08/276,887A

1994

Diskette,

3 - 1/2

inch

of America

Linear

Double-stranded

pairs

Genomic

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; ORGANISM: US-07-914-282D-3
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Similarity 48.0%;
)7; Conservative
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Pred. No. 0.036;
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Best Local Similarity
Matches 107; Conser
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ORGANISM:
-08-276-887A-3
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TITLE OF INVENTION: MICROBIAL DI
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Flavobacterium s
                                 TELEFAX: (503) 220 377
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: March 23, 199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: July 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William D. Noonan, M
                                                                    NAME: William D. Noonan, M.D. REGISTRATION NUMBER: 30878
REFERENCE/DOCKET NUMBER: 2815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
                                                                                                                                                                                                                                                                                                                                      ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM PC comp

OPERATING SYSTEM: MS
                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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ANTI-SENSE:
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STREET: 121 S.W
STREET: Suite 10
CITY: Portland
STATE: Oregon
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              TYPE: |
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CLASSIFICATION:
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TYPE: NUCLEIC STRANDEDNESS:
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One World Trade (
121 S.W. Salmon |
Suite 1600
                           1432
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March 23, 1992
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Double-stranded
                           pairs
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Street
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                                                                                                                   2815-36746-WDN
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ENZYMES INVOLVED
DEGRADATION OF PI
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US-08-997-080-169
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PCT-US93-02460-3
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Best Local Similarity 48.0%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5968524
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                INFORMATION FO
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                                                                                                                                                                   APPLICATION
FILING DATH
ATTORNEY/AGEN
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TITLE OF I
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                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,
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NUMBER OF SE
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                                                  SEQUENCE CHA
                                                                                                                  TELECOMMUNIC
                                                                                                                                                                                                            PRIOR APPLIC
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                          REGISTRATI
                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                        TELEFAX:
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                                                                                                                                                        AGENT INFORMATION: Sleath, Janet
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                                                                                     leath, Janet
ITION NUMBER: 37,007
E/DOCKET NUMBER: 11000.1007
IICATION INFORMATION:
E: 206-269-0565
                                                                                                                                                                                                                                                                                   YPE: Diskette
: IBM Compatible
: SYSTEM: DOS
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                                                                                                                                                                                                                        ATION:
                                                                                                                                                                                                                                                                                                                                                                                  ittle
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2601 Elliott Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAN, PAUL L.J.
ENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
QUENCES: 194
                                                                R SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                N NUMBER:
                                                                                                                                                                                                            ATION DATA:
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Suite 4185
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US-08-997-362-169
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Best Loc
Matches
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                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent AJ
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent AJ
FILING DATE: August 29, 1996
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.100
                           INFORMATION
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APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOU
TITLE OF INVENTION: TREATM
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of
STREET: 2601 Elliott Ave
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APPLICANT:
SEQUENCE (
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                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
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11 Similarity 46.2%;
121; Conservative
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           V FOR SEQ ID NO:
CHARACTERISTICS:
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Visser, Elizabeth
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TREATMENT
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Pred. No. 0.066;
0; Mismatches 14
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Suite 4185
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; TYPE: nucleic acid; STRANDEDNESS: sing; TOPOLOGY: linear US-08-997-362-169
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US-09-095-855-169
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
CLASSIFICATION DATA:
APPLICATION UMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
FILING DATE: 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUE
CORRESPONDENCE
ADDRESSEE: L
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                                                                 FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/9
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        ZIP: 98121
COMPUTER READABLE FORM:
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TELECOMMUNI
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REGISTRAT
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CITY: S
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Local Similarity
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                                                          leath,
E/DOCKET NUMBER: 11000.1002c3 ICATION INFORMATION: E: 206-269-0565
                                          leath, Janet
FION NUMBER:
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Skinner, Margot
Prestidge, Ross
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Pred. No. 0.066;
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rife: nucleic acid; STRANDEDNESS: single; TOPOLOGY: linear US-09-095-855-169
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US-09-324-542-169
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APPLICANT: Tan, Paul L.J.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the TITLE OF INVENTION: of Immunologically-Mediated Sk:

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 169

LENGTH: 1111
                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 121
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GENERAL INFORMATION:
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Best Local Similarity 46.2%;
Matches 121; Conservative
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SEQUENCE
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TYPE: DY
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9-324-542-169
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5. 6328978
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RESULT 9
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CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-11

EARLIER FILING DATE: 1997-12-23

EARLIER APPLICATION NUMBER: 08/873,970

EARLIER FILING DATE: 1997-06-12

FARLIER FILING DATE: 1997-06-12
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US-08-997-080-93
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EARLIER APPLICATION NUMBER: (
EARLIER FILING DATE: 1996-08-
NUMBER OF SEQ ID NOS: 200
SOFTWARD
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                                                                                                Sequence 93, Applicat Patent No. 5968524
GENERAL INFORMATION:
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TITLE OF INVENTION: Diagnosis
FILE REFERENCE: 11000.1002c4
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9-205-426-169
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                                         APPLICANT: WATSON, APPLICANT: TAN, PAU TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                             CORRESPONDENCE
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601 Elliott Avenue,
                                         QUENCES:
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Law Offices of Ann W. Speckman
)1 Elliott Avenue, Suite 4185
                             ADDRESS:
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                                                      PAUL L.J.
N: METHODS
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Pred. No. 0.066;
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                                                         AND COMPOUNDS
                                                          FOR
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US-08-997-362-93
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                                                                                                           Sequence 93, A Patent No. 598 GENERAL INFOR APPLICANT:
APPLICANT:
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APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS A
TITLE OF INVENTION: TREATMENT A
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
8-997-080-93
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0563
TELEFAX: 206-269-0563
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APPLICATION NUMBER: US/^^
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                   APPLICANT:
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Local Similarity 46.2%;
nes 121; Conservative
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                                                                                                                                                     93, Application 5985287
                                                                                                                                          INFORMATION:
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                                                                               Hiyama, Jun
Visser, Elizabeth
Skinner, Margot
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No. 0.072;
                              METHODS FOR DIAGNOSIS OF
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                                MYCOBACTERIAL INFECTIONS
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Seque...
Patent No. 600110N:
Tan, F

APPLICANT:

Paul

APPLICANT: APPLICANT:

Hiyama, Jun Visser, Elizabeth Skinner, Margot Scott, Linda Prestidge, Ross

APPLICANT:

Sequence

93, Application US/08873970 ). 6001361

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; STRANDEDNESS:
; TOPOLOGY: lii
; MOLECULE TYPE:
US-08-997-362-93
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RESULT 12
US-08-873-970-9
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APPLICATION NUMBER: U.S. Paten
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Paten
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ
SEQUENCE CHARACTER
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STREET: 2
CITY: Sea
STATE: WI
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Local Similarity 46.2%;
nes 121; Conservative
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: 2601 Elliott Avenue, Suite 4185
Seattle
WA
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                                                  SCGGTGGTAGTGCCGAT 1240
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/DOCKET NUMBER: 11
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FastSEQ for Windows Version
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RESULT 13
US-09-095-855-93
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Best Local S
Matches 121
                                       Sequence 93, Application Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
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INFORMATION FOR
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APPLICATION NUMBER: 08/705
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,00
REFERENCE/DOCKET NUMBER: 1
   APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 1341 base pair:
TYPE: nucleic
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873
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TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
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ADDRESSEE: Law Offices of
STREET: 2601 Elliott Avenu
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CITY: Seattle
STATE: WA
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ZIP: 981
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OF INVENTION:
OF SEQUENCES:
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121; Conser
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Tan, Paul
Visser, Elizabeth
Skinner, Margot
Prestidge, Ross
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Pred. No. 0.07
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0.072;
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RESULT 14
US-09-324-542-93
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; Patent INFORMATION:
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Best Local
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. S

STREET: 2601 Elliott Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: 09-095-855-93
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APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
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COMPUTER READAB
MEDIUM TYPE:
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OPERATING
SOFTWARE:
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STRANDEDNESS: single
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TITLE OF INVENTION: Diagnosis of Mycobacterial In
FILE REFERENCE: 11000.1002c4
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER APPLICATION NUMBER: 08/873,970
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APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and C.
TITLE OF INVENTION: of Immunologi
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08
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NUMBER OF SEQ ID NOS: 194
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-10-124-800-	S-09-745-763-	-10-124-800-17	-09-976-059-1	S-09-815-242-9	S-10-023-523-17	S-10-023-529-1	S-09-962-055-1	-09-976-740-17	S-10-023-523-4	S-10-023-529-4	-09-976-740-46	S-09-070-927A-3	S-09-815-242-14	S-09-815-242-13	US-09-815-242-112	S-09-815-242-64	S-09-815-242-381	S-09-815-242-87	-09-880-505-93	-10-051-643-93	-09-880-505-16	-10-051-643-16	S-10-023-523-1	S-10-023-529-1	S-09-962-055-1
1, App	Sequence 198	17,	equence 1, Appl	e 9579,	17,	Sequence 17, Appl	ce 17,	17, A	e 46,	e 46, Ā	4	e 367,	e 147,		e 112,	e 6463,	e 3815, Ā	ce 87	io O	equence 93,	equence 169	equence 169	14, Ap	e 14, Ap	Sequence 14, Appl

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## ALIGNMENTS

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ESULT 1 S-09-736-969A-1 Sequence 1, App

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APPLICANT: LU, Peter
APPLICANT: Garman, Jonathan David
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: CLASP-4 Transmembrane p
FILE REFERENCE: 020054-000411US
CURRENT APPLICATION NUMBER: US/09/736,969A
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
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PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR APPLICATION NUMBER: US 60/240,503
PRIOR APPLICATION NUMBER: US 60/240,503
PRIOR APPLICATION NUMBER: US 60/240,508
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,508
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PRIOR APPLICATION NUMBER: US 60/240,508
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Patent No. US20020068302A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter
APPLICANT: Garman, Jonathan David
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APPLICA

ATION NUMBER:

60/170,453

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RESULT 2
US-09-736-969A-7
; Sequence 7, Application US/09736969A
; Patent No. US20020068302A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Garman, Jonathan David
; APPLICANT: Candia III, Albert Freder
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APPLICANT: Garman, Jonathan David APPLICANT: Candia III, Albert Frede APPLICANT: Arbor Vita Corporation TITLE OF INVENTION: CLASP-4 Transmem FILE REFERENCE: 020054-000411US CURRENT APPLICATION NUMBER: US/09/73 CURRENT FILING DATE: 2000-12-13 PRIOR APPLICATION NUMBER: US 60/160, PRIOR FILING DATE: 1999-10-21 PRIOR APPLICATION NUMBER: US 60/162, PRIOR APPLICATION NUMBER: US 60/162, PRIOR FILING DATE: 1999-10-29
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Matches
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NAME/KEY: CDS
LOCATION: (95)..(6121)
OTHER INFORMATION: human
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NUMBER OF
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Local Similarity 71.8%;
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rt Frederick
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Pred. No. 2.6e-74;
); Mismatches 141;
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LOCATION: (4
OTHER INFORM
-09-736-969A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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422
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Local Similarity 71.2%;
nes 356; Conservative
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OR APPLICATION NUMBER: US 09/547,276

OR FILING DATE: 2000-04-11

OR APPLICATION NUMBER: US 60/196,267

OR FILING DATE: 2000-04-11

OR APPLICATION NUMBER: US 60/196,460

OR FILING DATE: 2000-04-11

OR APPLICATION NUMBER: US 60/196,527

OR APPLICATION NUMBER: US 60/196,527

OR FILING DATE: 2000-04-11

OR APPLICATION NUMBER: US 60/196,528
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APPLICATION NUMBER: US
FILING DATE: 2000-10-13
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APPLICATION NUMBER: US (
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APPLICATION NUMBER: US (
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APPLICATION NUMBER: US 09/687,837
FILING DATE: 2000-10-13
APPLICATION NUMBER: US 60/240,503
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                                                                                                                                                                                                                                                                                                            CTGAT
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                                                                                                            CCCGAGCTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGAT
                                                                                                                                                       AACGACCCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACG
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                            TTTTC
                                                                                 GACTTAACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAG
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RMATION: human CLASP-4
AGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATCGAC
                           AGAGGCTGCGATGTTATGTCCATGTAGCAGCTCTAGTTGCAGAGTTTCTTCAT
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ATION NUMBER: US 60/196,528
DATE: 2000-04-11
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NUMBER: US 6
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           Query Match 26.1%;
Best Local Similarity 78.1%;
Matches 157; Conservative
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TITLE OF II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864, /CCURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207, 456
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EQ ID NO 13960
LENGTH: 483
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                                                                      OTHER INFORMATION:
OTHER INFORMATION:
09-864-761-13960
                                                                                                                  FEATURE:
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PRAPPLICATION NUMBER: PCT/US01/00668
PREFILING DATE: 2001-01-30
PRAPPLICATION NUMBER: PCT/US01/00663
PREFILING DATE: 2001-01-30
PRAPPLICATION NUMBER: PCT/US01/00662
PREFILING DATE: 2001-01-30
PRAPPLICATION NUMBER: PCT/US01/00661
PRAPPLICATION NUMBER: PCT/US01/00670
PRAPPLICATION NUMBER: PCT/US01/00670
PRAPPLICATION NUMBER: PCT/US01/00670
PRAPPLICATION NUMBER: US 60/234,687
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OTHER INFORMATION: full length human CLASP-7 cDNA
NAME/KEY: CDS
LOCATION: (13)..(6156)
OTHER INFORMATION: human CLASP-7
JS-09-736-968A-1
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TYPE: DNA
ORGANISM: Homo sapiens
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PLICANT: Chen, Wensheng
TLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACI
TLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
THE OF INVENTION NUMBER: US/09/864,761
TRENT APPLICATION NUMBER: US 60/180,312
TOR APPLICATION NUMBER: US 60/207,456
TOR APPLICATION NUMBER: US 60/207,456
TOR FILING DATE: 2000-05-26
TOR APPLICATION NUMBER: US 09/632,366
TOR APPLICATION NUMBER: GB 24263.6
TOR APPLICATION NUMBER: GB 24263.6
TOR APPLICATION NUMBER: US 60/236,359
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0524, Application US/09864761
US20020048763AI
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CATION NUMBER: US 6
G DATE: 2000-10-13
EQ ID NOS: 115
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L, David K.
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; Sequence 3, Application US/U
Patent No. US20020102267A1

GENERAL INFORMATION:

APPLICANT: Lu, Peter

APPLICANT: Garman, Jonathan David

APPLICANT: Candia III, Albert Frederick

APPLICANT: Arbor Vita Corporation

TITLE OF INVENTION: CLASP-5 Transmembrane Pr

FILE REFERENCE: 020054-000511US

CURRENT APPLICATION NUMBER: US/09/736,960

CURRENT FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/160,860

PRIOR FILING DATE: 1999-10-21

PRIOR APPLICATION NUMBER: US 60/162,498
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ORGANISM:
FEATURE:
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Local Similarity
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DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00668

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00663

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00662

DR APPLICATION NUMBER: PCT/US01/00661

DR APPLICATION NUMBER: PCT/US01/00670

DR APPLICATION NUMBER: PCT/US01/00670

DR FILING DATE: 2001-01-30

DR APPLICATION NUMBER: US 60/234,687

DR APPLICATION NUMBER: US 09/608,408

DR FILING DATE: 2000-06-30

DR APPLICATION NUMBER: US 09/774,203

DR APPLICATION NUMBER: US 09/774,203

DR APPLICATION NUMBER: US 09/774,203

DR FILING DATE: 2001-01-29

BER OF SEQ ID NOS: 49117
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R APPLICATION NUMBER: PCT/US01/0/
R FILING DATE: 2001-01-30
//R APPLICATION NUMBER: PCT/US01/0//
//R FILING DATE: 2001-01-30
//R APPLICATION NUMBER: PCT/US01/0///
//R APPLICATION NUMBER: PCT/US01/0////
//R FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
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EST_HUMAN HIT: BE896788.1, EVALUE 9.00e-

SWISSPROT HIT: O24696, EVALUE 3.90e-01

NT HIT: gill429300, EVALUE 6.00e-93
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Pred. No. 4e-2
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; OTHER INFORMATION: human CLASP-5
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LING DATE: 2001-03-01
ICATION NUMBER: 60/186,126
NG DATE: 2000-03-01
ICATION NUMBER: 60/190,479
ICATION NUMBER: 60/200,545
ICATION NUMBER: 60/200,545
ICATION NUMBER: 60/200,303
ICATION NUMBER: 60/200,303
NG DATE: 2000-04-28
ICATION NUMBER: 60/200,779
NG DATE: 2000-04-28
ICATION NUMBER: 60/200,999
ICATION NUMBER: 60/200,999
NG DATE: 2000-05-01
ICATION NUMBER: 60/202,084
NG DATE: 2000-05-04
ICATION NUMBER: 60/206,201
NG DATE: 2000-05-04
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ICATION NUMBER: 60/218,950
ICATION NUMBER: 60/218,950
ICATION NUMBER: 60/218,950
                                                                                                                                                                                                                     IG DATE: 2000-08-04
CATION NUMBER: 60/223,378
IG DATE: 2000-08-07
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5465
                                                                                              15.8%;
milarity 53.4%;
Conservative
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ATION NUMBER: 60/222,903
DATE: 2000-08-03
ATION NUMBER: 60/223,416
CCAGGTGGAGGAACTTCTCTGTAATCTGAATAGCATCTTATATGACACAGTGAAA
                       TGATGTGAAGGACTTAACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAG 226
                                                GAGGACAATTTTGGCCTATTCAGAAGAGGACACAGCCATGCAGATGACTCCTTTT 69
                                                                       GTCCATCATCAACAACTGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTC 166
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ligate, Paul A.
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US20020198362A1
                                                                                                                                                                                                               Windows Version 3.0
                                                                                               Score 79.4; DB 9;
Pred. No. 6.3e-15;
0; Mismatches 146
                                                                                                    146;
                                                                                                                           Length 427;
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CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2001-COPRIOR APPLICATION
   Query
                                       NAME/KEY: unsure
LOCATION: (404)
OTHER INFORMATION:
NAME/KEY: unsure
LOCATION: (411)
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                                                                                                             ORGANISM: FEATURE: NAME/KEY:
                                                                                       LOCATION: (371)
OTHER INFORMATION:
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R APPLICATION NUMBER: 60/202,08
R FILING DATE: 2000-05-04
R APPLICATION NUMBER: 60/206,20
R FILING DATE: 2000-05-22
R FILING DATE: 2000-05-22
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DATE: 2000-08-0,
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TIME DATE: 2000-08-03
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R OF SE(
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R APPLICATION NUMBER: US 60
R FILING DATE: 1999-10-21
R APPLICATION NUMBER: US 60
R FILING DATE: 1999-10-29
R APPLICATION NUMBER: US 60
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R APPLICATION NUMBER: US 60
R FILING DATE: 2000-01-14
R APPLICATION NUMBER: US 60
R FILING DATE: 2000-02-14
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R APPLICATION NUMBER: US 60
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INVENTION: CLASP-7 Transmer
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NOS: 115
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SI
TITLE OF INVENTION: GENE EXPRESSION ANALYS
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-09-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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Best Local Similarity 56.7%;
Matches 106; Conservative
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TYPE: DNA
ORGANISM: Homo
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FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-
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LICATION NUMBER: US 09/608,408
ING DATE: 2000-06-30
LICATION NUMBER: US 09/774,203
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GENERAL INFORMATION:

APPLICANT: Lu, Peter

APPLICANT: Garman, Jonathan David

APPLICANT: Candia III, Albert Frederick

APPLICANT: Arbor Vita Corporation

TITLE OF INVENTION: CLASP-5 Transmembrane Pr

FILE REFERENCE: 020054-000511US

CURRENT APPLICATION NUMBER: US/09/736,960

CURRENT FILING DATE: 2001-09-20

CURRENT FILING DATE: 2001-09-20
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DR APPLICATION NUMBER: PCT/US01/00670

DR APPLICATION NUMBER: US 60/234,687

DR APPLICATION NUMBER: US 60/234,687

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EXPRESSED IN BONE MARROW, SIGNAL

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PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
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VERSION

BQ434370.1 GI:21173446

KEYWORDS

SOURCE

ORGANISM

EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

I (bases 1 to 869)

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

JOURNAL

COMMENT

Tissue Procurement: AFCC

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:

http://image.llnl.gov

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EVA13750.1 GI:21173446

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Mammalia; Eutheria; Primates;
1 (bases 1 to 994)
NIH-MGC http://mgc.nci.nih.go
National Institutes of Health
Unpublished (1999)
Contact: Robert Strausberg, P
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Tech
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AGENCOURT_6792185 NIH_MGC_1
5', mRNA sequence.
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/db_xref="taxon:9606"
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/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; S:Site_2: Sall; Cloned unidirectionally. P:Average insert size 1.75 kb. Library contectional contection contection contection contection contection contection contection contection contection contection contection content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content 
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493; Conservative
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12829 row: j column: 04
High quality sequence stop: 499.
                                                                                                    AGAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCAC
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/db_xref="taxon:9606"
/clone="IMAGE:5768931"
/clone="IMAGE:5768931"
/clone=lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

74 a 255 c 244 g 220 t 1 others
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Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria;
1 (bases 1 to 454)
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418; Conser
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BE163028.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-HT0457-070 300-113-c03&t3=2000-03-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 454.
Location/Qualifiers

1 /5/
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Shotgun sequencing of the human transcriptome with ORF sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                    Conservative
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/db_xref="taxon:9606"
/clone_lib="HT0457"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
38 a 112 c 124 g 130 t
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Primates;
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Pred. No. 1.4e-107;
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TGCTAA
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Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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e: LLCM1651 row:
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Location/Qualifiers
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
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/note="Organ: prostate; Sfil (ggccattatggcc); Site_1: Glontech
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/note="Organ: prostate; Sfil (ggccattatggcc); Site_2: Sfil (ggccattatggcc);
/note="Organ: prostate; Sfil (ggccattatggcc);
/note="Organ: prostate; Sfil (ggccattatggcc);
/note="Organ: postate; Sfil (ggccattatggcc);
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/note="Organ: postate; Sfil (ggccattatggcc);
/note="Organ: postate; Sfil (ggccattatggcc);
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Procurement: DCTD/DTP
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/db_xref="taxon:9606"
/clone="IMAGE:4804592"
/clone_lib="NIH_MGC_60"
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/db_xref="taxon:
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Best Local Similarity 87.6%;
Matches 438; Conservative
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 62
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National Institutes of Health, Mammalian Gene Collectic Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11878 row: m column: 07
High quality sequence stop: 693.
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                          CTGATAGCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATC
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603309631F1 NCI_CGAP_Mam6 MmRNA sequence.
BI691316
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EST.
house mouse.
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Mammalia; E
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                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345838"
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                           Ø
                                                                                                                                                       /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa. Site_2: NotI; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
182 c 191 g 146 t 1 others
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Rodentia;
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLAM11949 row
High quality sequence
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1-MGC http://mgc.nci.nih.gov/.
ional Institutes of Health, Mammalian
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                    Expressed genes in X. laevis emb
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Info
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411
                                                                                                                            African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chu
Amphibia; Batrachia; Au
Xenopodinae; Xenopus.
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laevis cDNA
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Fax:
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                      1 Yata, Mishima, Shizuoka 41: 81-559-81-6856
1: 81-559-81-6855
1: tshini@genes.nig.ac.jp.
Location/Qualifiers
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NIBB Mochii normalized Xenopus tailbud l
DNA clone XL091d16 5', mRNA sequence.
/organism="Xenopus laevis
/db_xref≈"taxon:8355"
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., To
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/clone_lib="NIBB Mochii normalized
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/dev_stage="stage 25"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It(
x,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
x,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
x,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
x,M., Konno,H., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
x,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
x, RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res
10 (11), 1757-1771 (2000)
x, And Hayashizaki,Y., Shibata,K., Itoh,M., Carninci,P., Sugaha
y, and Hayashizaki,Y.
TACACTGGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAG
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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e mouse tissues
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/db_xref="taxon:10090"
/clone="9530048J06"
/clone_lib="RIKEN full-length enriched,bladder"
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
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/dev_stage="adult"
/lab_host="DH10B"
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National Cancer I
Tumor Gene Index
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AW909665.1
                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng F
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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Other_ESTs: ur72d11.x1
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                                                                                                               ity sequence stop:
Location/Qualifiers
                                           /oryanism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:3155829"
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/dev_stage="10 months
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                                      /clone_lib="NCI_CGAP_Mam3"
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Best Local Similarity 87.8%;
Matches 360; Conservative
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                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina 1 (bases 1 to 520)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (Murina)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car found through the I.M.A.G.E. Consortium/LLNL at:
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BE533728
BE533728.1 GI:9762373
EST. house mouse.
                                   http://image.llnl.gov
Plate: LLAM8774 row:
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quality sequence stop: Location/Qualifiers
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Pred. No. 9e-83;
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Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 922)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ424615 922 bp rAGENCOURT_7834017 NIH_MGC_67 Homo sa 5', mRNA sequence.
BQ424615 BQ424615.1 GI:21119930 EST.
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/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

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/clone="IMAGE:3596515"
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sapiens cDNA clone
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Eukaryota; Metazoa; Chordata; Craniata; Ver

Mammalia; Eutheria; Rodentia; Sciurognathi;

1 (bases 1 to 871)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Ge

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.

cDNA Library Preparation: Life Technologie

cDNA Library Arrayed by: The I.M.A.G.E. Co

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution
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Plate: LLAM13492 row: e column: 19
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/clone="IMAGE:6153210"
/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Sisite_2: Sall; Cloned unidirectionally. Prayerage insert size 1.75 kb. Library correctionologies."
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                      sapiens
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/db_xref="taxon:10090"
/clone="IMAGE:5148461"
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/dev_stage="7 months"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-RT0067.150101-538-a01&t3=2001-01-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 584.
Location/Qualifiers
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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/db_xref="taxon:9606"
/clone_lib="RT0067"
/dev_stage="Adult"
/note="Organ: kidney_tumor; Vector: pucl8; Site_1: SmaI;
/note="Organ: kidney_tumor; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Email: cgapb
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://image.llnl.gov
s clone was contributed by the Brain Molecular Anatomy Project
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/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

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Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:10090"
/clone="IMAGE:5703138"
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/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage re
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12347 row: b column: 24

High quality sequence stop: 685.

Location/Qualifiers
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                           TGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTAACCAAAAGGAT
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5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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/db_xref="taxon:9606"

/clone="IMAGE:5583671"

/clone_lib="NIH_MGC_92"

/tissue_type="embryonal carcinoma, cell line"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally; oligo-dT primed.

Site_2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 2.5 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

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Perfect score:
Sequence: Minimum Maximum Run OM nucleic Searched: Database Post-processing: Scoring table: on: number DB DB seq seq of nucleic search, GenEmbl:\*

1: gb\_ba:\*
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# SUMMARIES

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### ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX255048	17 E C C E + +
Angiogenesis-associated proteins, and nucleic acids encoding the		1 (bases 1 to 7506)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	etazoa; Chordata; Craniata; Verte	Homo sapiens	human.		AX255048.1 GI:16074541	AX255048	Sequence 7 from Patent W00170808.	AX255048 7506 bp DNA linear PAT 10-0CT-2001	•	
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 3899)
Yue, H., Tang, Y.T., Hillman, J.L., Lal, P., I
Azimzai, Y., Yang, J., Reddy, R. and Lu, D.A.
Human intracellular signaling molecules
Patent: WO 0077040-A 90 21-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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n Corporation (US); GENENTH
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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GAAATCATGCATGAGCAGATCTGCCCCCTGGAGGA-GAAGACGAGCGTCTTACCGAATTC
                                                                                                                                                                                                                                                                                                       CCTTCACATCTTCAACGCCATCAGTGGGACTCCAACAAGCACAATGGTTCACGGGATGACCCTTCACATCTTCAACGCCCATCAGTGGGACTCCCAACAAGCACAATGGTTCACGGGATGACCCTTCACATCTTCAACGCCCATCAGTGGGACTCCCAACAAGCACAATGGTTCACGGGATGAC
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                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 7522)
1 (bases 1 to 7522)
                                                                                                                                                                                                                                        o sapiens zizimin1 mRNA,
27605
       /note="guanine nucleotide
activator"
                                 /organism="Homo sapiens
/db_xref="taxon:9606"
/chromosome="13"
                                                                                                                                                                                                                                 GI:22038158
                           . 6265
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99.8%;
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Pred. No. 3.9e-130;
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Jolla, CA
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                                                                                                   CTTTGTCATTTGCAAACTCAGGATGCTTTCCAAAGCCAATCACTGGGGAGACCGAGCACA
                                                                                                                                                                                                            GGATGACCAGCTCGTCTTCGGTCGTGTGATTACATCTCATGGCCCGTGTGTGGGGACTTG
GGGAGGACC-AGGGGAAGGGAGAGAAAGGAAATAAAGAACAACGTTATTTCTTAACAGA
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similarity 98.2%;
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NSCHSTENSELNDETISBECLHKGYTTALDTLLKFSADHLATKKSLLAVFI
KRGRIGKYGLLANIATEVULTFALDTLSLTFYKFBFTYSCTAADKCHALDGHGHPLJMKKVPDVY
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KAERYNEDSTALKSVTATTALDTLSLATHVOLTSLANSLTTENST
VARFCASCYPSCOLKRPIILTALTCLTAATATALDLDGGTTFDLLECCADCHK
KAERYNEDSTALLTURGSTDYDGFERLAHLYCTTALTDTLKKYEDDLLAVSKYSTEV
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..2e-124;
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Mammalia; E
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Homo sapiens mRNA for KIAA1058 p
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AB028981.2 GI:20521745
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DKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSDFPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained bysubcloning of the DNA
fragments derived from two cDNA clones (1 - 1846 was
derived from ef00877 and 1847 - 7545 was derived from
hh12146)."
1. .7545
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Eutheria;
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YVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQK
SFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEI
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/codon_s
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'chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase, T.,
Kotani, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brain cDNA to mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishikawa, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirosawa, M., Miyajima, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partial cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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RESULT 5
AL357553/c
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ORIGIN
                                           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAATTCCCTTCACATCTTCAACGCCATCAGTGGGACTCCAACAAGCACAATGGTTCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATCATGCATGAGCA------GATCTGCCCCCTGGAGGAGAAGACGAGCGTCTTAC
                                                                                                                                                                                                                                                            GGGAGGACCAAGGGGAAGGGAGAGAAAGGAAATAAAGAACAACGTTATTTCTTAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGTCATTTGCAAACTCAGGATGCTTTCCAAAGCCAATCACTGGGGAGACCGAGCACA
                                                                                                                                                                           AAGTTTTCATTGTGTCTTAACAAAGGTGT
                                                                                                                                                                                                 AAGTTTTCATTGTGTCTTAACAAAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 98. 500; Conservative
Homo sapiens chromosome PROGRESS ***, 2 unordere AL357553
                                                                AL357553
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FFQYCQKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVA
VNVTRVIIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELIKSMTTILKP
SADFLTSNKLLKYSWF FFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAVETVVNML
MPHITQKFRDNPEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLF
EYKFEFLRVVCNHEHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLR
EVGTALQEFREVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQ
RINVRDVSPFPVNAGMTVKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASP
YTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDK
LDQSEIKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRY
IARTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSL
FTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFY
EGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII
SVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATA
QMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVT
ALVAEYLTRKEAVQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMME
DVGMQDVHFNEDLLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMME
DVGMQDVHFNEDLLEQCADGLWKAAERYELIADIYKLIIPIYEKRRDFERLAHLY
DTLHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYI
YKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYXIQVTHVIPF
FDEKELQERKTEFERSHNIRRFMFEMFFTQTGKRQGGVEEQCKRRTILTAIHCFPYVK
KRIPVMYQHHTDLNPIEVAIDEMSKKVAELROLCSSAEVDMIKLQLKLQGSVSVQVNA
GPLAYARAFLDDTNTKRYDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEE
MKANYREMAKELSEIMHEQLG"
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98.2%;
              155198 bp
romosome 13 clone
unordered pieces.
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Pred. No. 1.2e-124;
0; Mismatches 0;
                                           clone
                                                                                                                                                                           6649
                                               RP11-56D6,
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                                              linear HTG 10-JUL-2001 *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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Best Matches

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KEYWORDS
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                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                  Query Match 72.9
Best Local Similarity 100
Matches 365; Conservative
                                                   130533
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                   257
                                                 CCATC
TGTGAT
                                                                                   CCATC
                                                                                                                                                  AGATC'
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                                                                                                                                                                                                                                                                                                                                                                      featu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peck, A.
Direct Subsubmitted
CB10 1SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL3575
HTG; H
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 152143 bases at least Q40
Consensus quality: 153069 bases at least Q30
Consensus quality: 153660 bases at least Q20
Insert size: 155098; sum-of-contigs
Insert size: 144134; 11.1% error; agarose-fp
Quality coverage: 5.59x in Q20 bases; sum-of-contigs Quality
coverage: 6.57x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requests: clonerequest@sanger.ac.uk
On Apr 12, 2001 this sequence version replaced gi:12956937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                 TGCCCCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACG 196
TTACATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCATTTGCAAACTCAGGAT
                                                  AGTGGGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ltted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTGS.
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2254 155198: contig of 152945
Location/Qualifiers
1. 155198
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-56D6"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                   vector_side:right"
34926 c 34669 g
                                                                                                                                                                                                                                                                                                                                     /note=".
2254. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GI:13620383
_PHASE1; HTGS_CANCELLED.
                                                                                                                                                                                                                                                                                                /note="assembly_fragment:02529
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 155198)
                                                                                                                                                                                                  72.9%;
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                                                                                                                                                                                                                                                                                                                                       assembly_fragment:00588"
155198
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                                                                                                                                                                                  0;
                                                                                                                                                                                                    Score 365; DB 2;
Pred. No. 6.2e-94;
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REFERENCE . AUTHORS
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                                                                                                                                                                                                                                                           On Oct 1, 2000 this sequence version replaced gi:10039689.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13

Mapping Group. Further information can be found at
                                                                                            Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13

This sequence is the entire insert of clone RP11-155N3 The true left end of clone RP11-318G11 is at 114983 in this sequence. The true right end of clone RP11-56D6 is at 42341 in this sequence. The true right end of clone RP11-551M18 is at 43464 in this sequence. The This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-155N3 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
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HTG; KIAA0694;
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (31-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human |
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                                                                                  //www.chori.org/bacpac/home.htm
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    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
                                                          Location/Qualifiers
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Eutheria; Primates;
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11460. 1157
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12682. 1207
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9869....
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9586. .9667
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4418. .462^
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3191. .3475
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3123. .30
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/note="L1ME repeat: matches 5569. .5651 of 9714. .9813
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/note="match: STS: Em:HSA272"....
3060. .3191
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/note="MLT1B repeat: matches 8.
9220. .9344
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3887. .4074
/note="L2 repeat: matches 1607
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/clone_lib="RPCI-11
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complement(14122. ...
/note="match: GSS: ]
14334. .14400
                                                                                          /evidence=not_experimer complement(16480)
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16511. .16637
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/gene="bA155N3.2"
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  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: i Column: 2
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Baylor College of Medicine Human Ge
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Ha
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., M
Richards, S., Gibbs, R.A.
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Strausberg,R.
Direct Submission
Submitted (05-JUN-2001)
Gene Collection (MGC), C
Institute, 31 Center Dri
USA
NIH-MGC Project URL: htt
Contact: MGC help desk
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
l (bases 1 to 2998)
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e Collection (MGC), Cancer Genomics Office, National Cancer
titute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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EACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSDIMREQICPLEEKTSVLPNSL
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Rattus norvegicus.
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and Cocozza, S.
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ol. 13, 75-83 (1994)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Fischer"
/db_xref="taxon:10116"
/cell_line="FRTL-"
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codon_start=2
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A., Monticelli,
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 278.8; DF Pred. No. 3.1e-60; Mismatches 1
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                                                                                                                                   ---TGGAGAGGACAAGCGTGCTACCAAATTCC
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e-69;
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                                                                                  Sequencing vector: M13; 0%

Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178021 bases at least Q40
Consensus quality: 178402 bases at least Q30
Consensus quality: 178402 bases at least Q20
Insert size: 181640; sum-of-contigs
Quality coverage: 11.19 in Q20 bases; agarose-fp
Quality coverage: 9.89 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKATYOTA; Metazoa; Chordata; Crania Mammalia; Eutheria; Rodentia; Sciuro 1 (bases 1 to 182640)

McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone Unpublished 2 (bases 1 *- 1.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGGAGTTGTAAGAAGGTGCACATATTTTTTTAAATCTCACTGGCAATATTCAAAGTTTT
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Mus musculus
SEQUENCE, 11
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Web site
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HTG; HTGS_P
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                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (04-JUL-2002) Parkway, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to McPherson, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mous
                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                      code:
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PHASE1; HTGS_DRAFT;
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 4276:
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contig of 461.

1: contig of 301 bp 1.

1: contig of 5301 bp 1.

1: contig of 8550 bp in length

141: gap of unknown length

1848: contig of 14707 bp in length

52177: gap of unknown length

52277: gap of unknown length

52277: gap of unknown length

75893: contig of 23616 bp in length

75993: gap of unknown length

113549: contig of 37556 bp in length

113649: contig of 63712 bp in length

113640: gap of unknown length

12177461: gap of unknown length

122177461: gap of unknown length

1322179301: gap of unknown length

202179461: gap of unknown length

13640: contig of 1740 bp in length

202179301: gap of unknown length

13640: contig of 3339 bp in len

Location/Qualifiers

1. 182640

'romosome="UNK"

"--"RP24-119M15"

"ame:Contig10"

"ame:Contig11"
                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig10"
4377. .8990
/note="assembly_name:Contig11"
9091. .14391
/note="assembly_name:Contig11"
14492. .23041
/note="assembly_name:Contig12"
14492. .37848
/note="assembly_name:Contig13"
23142. .37848
/note="assembly_name:Contig14"
37949. .52177
/note="assembly_name:Contig16"
75994. .113549
/note="assembly_name:Contig16"
113650. .177361
/note="assembly_name:Contig18"
177462. .179201
/note="assembly_name:Contig8"
179302. .182640
/note="assembly_name:Contig9"
179302. .182640
/note="assembly_name:Contig9"
179302. .182640
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                              Score 220.6; DB 2;
Pred. No. 2.8e-52;
); Mismatches 94;
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of read
Assembly program: Phrap; version 0.990319
Consensus quality: 203478 bases at least Q40
Consensus quality: 204725 bases at least Q30
Consensus quality: 205702 bases at least Q30
Insert size: 161000; agarose-fp
Insert size: 208272; sum-of-contigs
Quality coverage: 14.47 in Q20 bases; sum-of-cor
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2 (bases 1 to 3
McPherson, J.D. 6
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Eukaryota;
Mammalia; E
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Mus musci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-JUL-2002)
Parkway, St. Louis, MO
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McPherson, J.D. and Waterston, The sequence of Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: M_BB0115A22
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                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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USA
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48978: gap of unknown length
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66344: contig of 17366 bp in 16
345
66444: gap of unknown length
98995: contig of 32551 bp in 16
99095: gap of unknown length
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116396: contig of 17301 bp in 16
1897
116496: gap of unknown length
135389: contig of 17301 bp in 16
1890
135489: gap of unknown length
155607: contig of 20018 bp in 16
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209372: contig of 3765 bp in 16
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116497. .135389
/note="assembly_name:Contig20"
135490. .155507
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13096. .23730
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REFERENCE
AUTHORS
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NOTE: This is a 'working draft' sequence. It currently consists of 75 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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2 (bases 1 to 192825)

Worley, K.C.
Direct Submission
Submitted (26-APR-2002) Human of Molecular and Human Genetic Baylor Plaza, Houston, TX 7703

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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GVFP
Center clone name: CH230-473M19
Center clone vector: Plasmid;
Chemistry: Dye-terminator Big Dye:
Assembly program: Phrap; version 0.
Consensus quality: 117932 bases at
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Hashimoto, K., Osada, N., Hida, M.,

Direct Submission

Submitted (09-MAR-2001) Katsuyuki Hashimoto, Nat.

Infectious Diseases, Division of Genetic Resource

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

7120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                            Terao, K., Hida, M., Kusuda, J., Ta
Terao, K., Suzuki, Y., Sugano, S. a
Isolation of full-length cDNA cl
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                                                                                        1-chome, Shinjuku-ku, Tokyo 10
(E-mail:khashi@nih.go.jp, URL:
Tel:81-3-5285-1111(ex.2120), F
Lab host: TOP10
Vector: pME18S-FL3 (Acc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb.The SfiI-digested PCR product was cloned
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Macaca fascicularis
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTATCATGAATGAGCAGCTCTGTC
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Ishii,S., Kav
Nakamura,Y.,
NEDO humar
                                                                                                                                                                   Homo sapien clone_lib:N Homo sapien Eukaryota;
                                                                                                                                                                                                                                                            AK001;
oligo
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simi
AK00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into distinct DraIII sites of pME18S-FL3. XhoI sites just the DraIII sites can be used to isolate the cDNA insert. were constructed by Sugano et al.(University of Tokyo, 1 Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAAGCTGCG]; 3' end primer [CGACCTGCAGCTCGAGCACA]).
                   Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suz
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwaya
                                                                                                                                                                                                                                                                                                                                                   AK00
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sapiens cDNA FLJ10391 fis,
lar to R.norvegicus trg mRNA
1253
                                                                                                                                                                                                                                                                                 1253.1
                                                                                                                                                                                                                         capping; fis (full insert sequence).
sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
_lib:NT2RM4 clone:NT2RM4000139.
           human cDNA
                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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LPIIRGKNALSNSKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEVCLTILDLLSLFT
QTHQRQLQQCDCQNSLMKRVFDTYMLFFQVNQSATALKHVFASLRLFVCKFPSAFFQG
PADLCGSFCYEVLKCCNHRSRSTQTEASALLYFFMRKNFEFNKQKSIVRSHLQLIKAV
SQLIADAGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLMATAQMK
EHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHIAALI
AEYLKRKGMFSMGWPAFLSITPNIKEEGAVQATDNPDNESPVPLREEENTSR"
- 588 c 570 g 749 t
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(CACCATGTG)"
191. .1525
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/clone_lib="macaque brain cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Macaca fascicularis
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                                                                                                                                                                      ; Metazoa; Eutheria;
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71.7%;
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                                                                                                                                                                      Chordata; Primates;
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Pred. No. 9.8e-12;
); Mismatches 41;
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                                                                               Murakawa, K.,
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                            Iwayanagi, T.
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Local Similarity 67.5%;
nes 110; Conservative
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E 2 (bases 1 to 2036)
E 2 (bases 1 to 2036)
S Isogai, T. and Otsuki, T.
Direct Submission
L Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'-& 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                          CAATTTGCAGATGCATGTGGGCAGGCCCTTGACGTGAATGAGCGCCTCATCAAAGAGGAC
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                                                                                                                                                                                                                                                                                                                              GAAATCATGCATGAGCAGATCTGCCCCCTGGAGGAGAAGACGA
                                                                 Eukaryota;
Mammalia; E
l (bases 1
   Direct Submission
Submitted (01-OCT-2001)
Gene Collection (MGC),
                                                                                                                 Homo
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                                                  Strausberg, R.
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BC015018
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TMEEVDMIRLQLKLQGSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFA
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CTRVISKATPALPTVSISSSAEV"
1 390 c 460 g 552 t
                                                                                ; Metazoa;
Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="teratocarcinoma"
/clone_lib="NT2RM4"
/note="cloning vector: pME18SFL3~mRNA from uninduced
neuronal precursor cells."
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/db_xref="taxon:9606"
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/cell_line="NT2"
                                                                  б
                                                                                                                                                                  GI:15929124
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MGC:8871
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Primates;
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   Cancer
                 National
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 Genomics Office,
                                                                                Craniata; V Catarrhini;
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i; Hominidae;
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                                                                                          CAGCT
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer
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NIH-MGC Project |
Contact: MGC hel
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Is clone was selected for full length sequencing because sed the following selection criteria: matched mRNA gi: Location/Qualifiers
                                                                                                                                                                            TGCAGATGCATGTGGGCAGGCCCTTGACGTGAATGAGCGCCTCATCAAAGAGGAC
CATGAATGAGCAGATTACGGGCAGGGACGACCTGTCAA
                                                                                       SGAGTACCAGGAAGAACTGAGGTCCCACTACAAGGACATGCTCAGCGAACTCTCC
                                                                                                                                                                                                                        TGTGGAAGCTTGCGGTCAAGCCTTAGCGGTAAACGAACGTCTGATTAAAGAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                   761
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                    /product="Unknown (protein for MGC:8871)"
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NENILVEQLYMCVEFLWKSERYELIADVNKPIIAVFEKQRDFKKLSDLYYDIHRSYLK
VAEVVNSEKRLFGRYYRVAFYGQGFFEEEEEGKEYIYKEPKLTGLSEISQRLLKLYADK
FGADNVKIIQDSNKVNPKDLDPKYAYIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFV
FETPFTLSGKKHGGVAEQCKRRTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEM
SKKVSELNQLCTMEEVDMIRLQLKLQGSVSVKVNAGPMAYARAFLEETNAKKYPDNQV
KLLKEIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMLSELSTVMNEQITGR
DDLSKRGVDQTCTRVISKATPALPTVSISSSAEV"
51 a 477 c 549 g 626 t
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/tissue_type="Skin, melanotic m
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/db_xref="taxon:9606"
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#### SUMMARIES

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DNA encoding cadherin-like asymmetry protein (CLASP) isoform #2.
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Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome; blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation; CLASP; gene; ss.

Homo sapiens.

W0200231117-A2.

18-APR-2002

15-OCT-2001; 2001WO-US32202.

13-OCT-2000; 2000US-0687837.

(ARBO-) ARBOR VITA CORP. (GARM/) GARMAN J D. (CAND/) CANDIA A F.

Lu PS;

WPI; 2002-416861/44. p-PSDB; ABG61673.

New human cadherin-like asymmetry protein(s) (CLASP)-2 for modulating an immune response, and for treating multiple sclerosis, rheumatoid arthritis, endometriosis, lupus, autoimmune thyroiditis, septic shock, and sepsis

Disclosure; Figure 3A; 245pp; English.

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                                                                       Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome; blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation;
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cc acid sequence that has 90 % sequence identity to one of the human cadherin-like asymmetry protein(s) (CLASP-2 A, 2B, 2C, 2E) cadherin-like asymmetry protein(s) (CLASP-2) (CLASP-2A, 2B, 2C, 2E) sequences (PS). (1) is useful for identitying a compound or agent that binds (CLASP-2 polypeptide. An antibody (II) to (I) is useful for cdetecting a CLASP-2 polypeptide in a sample. (II) is useful for comprising a nucleic acid encoding (I) or (II) is useful for comprising a nucleic acid encoding (I) or (II) is useful for comprising a nucleic acid encoding (I) or (II) is useful for preventing correcting a cLASP-2 polypucleotides are useful as probes or primers for correcting a clasp-2 polypucleotides are useful as probes or primers for detection or inhibition of CLASP-2 expression (e.g., antisense or clasp-2 expression), as a lymphocyte marker and for therapeutic polypucleotides or are used as therapeutic polypeptides, produce anti-CLASP-2 polypucleotides can be used in diagnostics (e.g., as probes or plynucleotides or fragments can be used in diagnostics (e.g., as probes or plynucleotides or polypucleotides can construct transgenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polypucleotides can screen for CLASP-2 agonists and antagonists. CLASP-2 polypucleotides can screen for CLASP-2 agonists and antagonists. CLASP-2 polypucleotides can increase differentiation and proliferation of haematopoietic cells, including the pluripotent stem cells to treat those cativation, differentiation of immune cells and can treat or detect deficiencies or disorders of haematopoietic selection of mamune cells and can treat or detect autoimmune diseases, e.g., Addison's disease, haemolytic anaemia, cells, including the pluripotent stem cells to treat those blood protein disorders (e.g., as pammaglobulinaemia, cells or polypeptides can treat or detect autoimmune diseases, e.g., Addison's disease, haemolytic anaemia, cells or polypeptides can treat or detect autoimmune diseases, e.g., Addison's di
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Matches
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361670.
adherin-like asymmetry protein(s) (CLASP)-2 for modulating esponse, and for treating multiple sclerosis, rheumatoid endometriosis, lupus, autoimmune thyroiditis, septic shock,
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                                                                100.0%; Score 501; DB 24; 100.0%; Pred. No. 3.8e-143; tive 0; Mismatches 0;
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                                                                                                                                                                                                         CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective; hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder; anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis; endometriosis; pregnancy induced hypertension; ss.
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99US-0134114.

99US-0134117.

99US-0134118.

99US-0160860.

99US-0162498.

99US-0170453.

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SXCCCCCCCCCCCCCCCCCXXXPPTXRR
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inflammatory responses
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P-PSDB; AAB36527.
                                                                                                                                               Example
                                                                                                                                                                      Isolated
                                                                                                                                                                 cadherin-like asymme ide used to diagnose,
                                                                                                                                               Fig 1; 286pp;
                                                                                                                                                                 asymmetry protein-2 polynucleotide and gnose, treat and prevent autoimmune di
                                                                                                                                               English.
                                                                                                                                                                    diseases
                                                                                                                                                                    and
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continflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the immune response in a subject by interfering with the capility of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an cantibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat chypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory crapense e,g, arthritis, inflammatory bowel disease and increase differentiation and proliferation of haematopoietic cells e.g. to treat chammatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence encodes human CLASP-2, which is used in the cexamplification of the present invention. The present (CLASP-2). C antiinflamma antianaemic, invention describes cadherin-like asymmetry protein-2 LASP-2 can have immunosuppressive, immunomodulatory,

VΩ Qy DЪ Qy Вb QУ B QУ δÃ B Дb δõ Дb Qy 밁 Qy g Query Ma Best Loc Matches 4100 4040 3920 860 800 980 181 121 361 301 241 equence 4 4 220 Loca 61 Match Local Sin es 501;  $\vdash$ CAGCTO CAATT CAAGG AGCTC GAAAT CAGCT CAATT TTTGCAAACTCAGGATGCTTTCCAAAGCCAATCACTGGGGAGACCGAGCACAGGGAGGAC AGCTC ATTGT GAAAT ATTGT CAAGGGGAAGGGAGAAAAGAAATAAAGAACAACGTTATTTCTTAACAGACTTTCTAT 4 807 GTCTTCGGTCGTGATTACATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCA CATGCATGAGCAGATCTGCCCCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCC CGAGTATCAGGAAGAAATGAAAGCCAACTACAGGGAAATGGCGAAGGAGCTTTCT 120 TGTGGAAGCTTGCGGTCAAGCCTTAGCGGTAAACGAACGTCTGATTAAAGAAGAC 60 milarity GTCTTAACAAAGGTGT GTCTTAACAAAGGTGT 501 GGAAGGGGAGAAAAGGAAATAAAGAACAACGTTATTTCTTAACAGACTTTCTAT Conservative BP; 1353 A; 1117 C; 1136 G; 1201 T; 0 other; 100.0%; 0; Score 501; DB 21; Pred. No. 3.8e-143; Mismatches 0 Length 4807; Indels 0,; Gaps 420 4099 4039 3979 180 3919 3859 480 4159 360 300 240

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RESULT 5
AAC87973
The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiarthritic, cytostatic, hypotensive, antirheumatic, cantiinflammatory, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the cability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and caugment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory cresponse e,g, arthritis, inflammatory bowel disease and increase chifferentiation and proliferation of haematopoietic cells e.g. to treat anaemia, thrombocytopaenia and other blood protein disorders. Disorders Disorders Disorders anaemia, thrombocytopaenia and other blood protein disorders. Disorders created by disrupting CLASP-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence encodes human CLASP-2A, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1999;
14-MAY-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated cadherin-like asymmetry protein-2 polynucleotide apolypeptide used to diagnose, treat and prevent autoimmune inflammatory responses -
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99US-0134114.

99US-0134117.

99US-0134118.

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                                                                                                      Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome; blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation;
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        2000US-0687837
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GARMAN J D.
CANDIA A F.
                                                           02-416861/44.
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           cadherin-like asymmetry protein(s) (CLASP)-2 for modulating response, and for treating multiple sclerosis, rheumatoid endometriosis, lupus, autoimmune thyroiditis, septic shock
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2). CLASP-2 can have immunosuppressive, immunomodulatory, lemic, haemostatic and neuroprotective activities. CLASP-2 can be inhibit an immune response in a subject by interfering with the response in a subject may also be inhibited by administering an ly which specifically binds to CLASP-2. CLASP-2 polynucleotides, is and antibodies can be used to prevent or treat a CLASP-2 is an autoimmune disease caused or exacerbated eased activity of TH11 cells. They can also be used to treat insittivities, prevent transplantation rejection responses and

The present inventions (CLASP-2). CLASP-antiinflammatory,

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Disclosure

Fig 10A; 286pp; English.

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P-PSDB; AAI
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                                                                                                                                        Isolated cadherin-like asymmetry protein-2 polyr polypeptide used to diagnose, treat and prevent inflammatory responses -
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         CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective; hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder; anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis; endometriosis; pregnancy induced hypertension; ss.
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99US-0162498.

99US-0170453.

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     3891
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99US-0162498.

99US-0170453.

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2000US-0182296.
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hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e,g, arthritis, inflammatory bowel disease and increase differentiation and proliferation of haematopoietic cells e.g. to treat anaemia, thrombocytopaenia and other blood protein disorders. Disorders treated by disrupting CLASP-2 function include multiple sclerosis, rheumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence represents a preliminary CLASP-2 nucleotide sequence, from the present invention.

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Score 501; DB 21; Pred. No. 3.9e-143; ; Mismatches 0;

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The present invention describes cadherin-like asymmetry process.

(CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antiinflammatory, antiinflammatory and immune response in a subject by interfering with the callity of a CLASP-2 can be used to inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 conceased activity of TH11 cells. They can also be used to treat hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit concease e.g. arthritis, inflammatory bowel disease and increase differentiation and proliferation of cells involved in an inflammatory response e.g. arthritis, inflammatory bowel disease and increase treated by disrupting CLASP-2 function include multiple sclerosis, concerning concerning chasp-2 function include multiple sclerosis, endometriosis and pregnancy induced hypertension. The present sequence represents a preliminary CLASP-2 nucleotide concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning concerning conc
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21-OCT-1999;
29-OCT-1999;
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14-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated cadherin-like asymmetry protein-2 polynucleotide and polypeptide used to diagnose, treat and prevent autoimmune diinflammatory responses -
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29-OCT-1999;
13-DEC-1999;
14-JAN-2000;
14-FEB-2000;
The present invention describes cadherin-like asymmetry protein-2 (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory, antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be used to inhibit an immune response in a subject by interfering with the ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated
                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                 polypeptide inflammatory
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US-08-232-463-14
US-08-923-137-2
US-09-056-075-2
US-09-255-829-7
US-08-405-496A-27
US-08-915-136-27
US-09-244-796-17
US-09-234-186-1
US-09-234-186-1
US-09-233-527-1
PCT-US93-05651-1
US-08-471-033-42
US-08-471-044-42
US-08-463-483A-39
US-08-471-046A-39
US-08-471-046A-39
US-08-470-566B-39
US-08-470-566B-42
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ESULT 2
US-09-484-970B-33
; Sequence 33, Application U
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen
; APPLICANT: Volkmuth, Way
; APPLICANT: Walker, Micha
; TITLE OF INVENTION: BONE
; FILE REFERENCE: PB-0014
; CURRENT APPLICATION NUMBE
                                                                                                                                                                                                                           ; Sequence 157, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
   APPLICANT: Benson, Darin R.
   APPLICANT: Mitcham, Jennifer L.
   APPLICANT: King, Gordon E.
   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OV.
   TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
   FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
   NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 157
; LENGTH: 1031
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; ORGANISM: HO
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  Volkmuth, Wayne
Walker, Michael G.
WENTION: BONE REMOI
ENCE: PB-0014 US
PLICATION NUMBER: US,
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US-08-471-033-45
US-08-471-044-45
US-08-463-483A-45
US-08-471-046A-45
US-08-471-0566B-45
US-08-471-033-27
US-08-471-044-27
US-08-470-566B-27
US-08-470-566B-27
US-08-470-566B-27
US-08-469-334-27
US-08-469-334-27
US-08-471-044-24
US-08-471-044-24
US-08-471-044-24
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Pred. No. 4.3e-33;
); Mismatches 5;
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Title: Perfect

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RESULT 3
US-08-232-463-14/c
; Sequence 14, Application U
; Patent No. 5670367
; GENERAL INFORMATION:
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         FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 33
LENGTH: 2225
TYPE: DNA
ORGANISM: Homo
FEATURE:
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NUMBER OF SEQ I
SOFTWARE: PERL
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OTHER INFORMATION:
09-484-970B-33
                                                                                                                                                                                                                                                            ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
APPLICATION NUMBER: EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
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STREET: 18
CITY: Alex
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Patent NC
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Best Local :
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                            NUMBER OF SEQUEI
CORRESPONDENCE I
ADDRESSEE: HO
                                                                                                                       ZIP: 19477
COMPUTER READAB
MEDIUM TYPE:
COMPUTER: IB
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APPLICANT:
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                                                                                         CURRENT APPLICATION DATA:
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STATE:
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SOFTWARE: Patent
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No. 6083716
AL INFORMATION:
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Pennsylvania
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                                                                                                                                             READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                        AAGGTGCACATAT 445
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                                                                             ION NUMBER:
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                                                                                                                                                                                                  Spring House Corporate
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                                                                                                                                                                                                                                                       Fisher,
                                                                                                                                                                                                                                                                  Farina,
                                                                                                                                                                                                                                                                              Wilson,
                                                                                                                                                                    United States
                                                                                                 PatentIn Release #1.0,
                                                                                                             :: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               Howson and Howson
                                                                                                                                                                                                                          ADDRESS:
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6.8%; Pred.
tive 213; Mi
                                                                                                                                                                                                                                             James M.
Steven F.
Krishna J.
Chimpanzee Adenovirus
                                                                             US/08/923,137
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                                   60/024,700
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pred. No. 0.012;
                                                                                                                                                                     America
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                                                                                                     Version #1.30
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US-09-056-075-2/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                   TELEFAX: 608-251-510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS: 2570 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 215-540-920
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36519 base pai
                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMAT
MOLECULE TYPE: -056-075-2
                                                                                                                                                                                                                                      ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
MOLECULE TYPE
8-923-137-2
                                                                                                                                                                                                                      CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9192
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE
ADDRESSEE: (
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                TYPE: nucle
STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386 REFERENCE/DOCKET NUMBER: 9
                       TOPOLOGY:
                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                       STATE:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCATGAGCAGATCTGCCCCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2, Application 5955368
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                                                                                                      Madison
WI
                                               nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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Rood, Julian
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                        linear
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                                                                                                                                                                                                                                                                                                                                                                     ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9124
                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
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                                   double
                                                                                                                                                                                                                     DATA:
         (genomic)
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Pney Street
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US-09-25
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US-09-255-829-7
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                                                                                Query Match
Best Local
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Best I
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INFORMATION F
SEQUENCE CH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy d.

COMPUTER: IBM PC compo
                                                                                                                                                                                                                        NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
NFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W
REGISTER
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 00 /7 APPLICATE: 77
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                       FEATURE:
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                          325
                                                402
                                                                                                                                                                   TYPE: nucreacy STRANDEDNESS: TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462
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                                                                                                                                          NAME/KEY:
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  GGCAAT.
                         TTAACA
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I: Quinn, Conrad Padraig
I: Foster, Keith Alan
INVENTION: Recombinant To
                    ATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGT 501
                                                                    ilarity 58.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACATTCTTCCAAGATCAGTTGAATAAATTCTCTCAAATAATTTTGTAACTCCCT 1480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STERNE, KESSLER, GOLDSTEIN, & FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plication US/09255829
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                                                                                                                            CDS
1..2613
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                                                                                                                                                                             linear
                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                        double
                                                                               58.0%;
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58.0%;
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                                                                  Score 32.8; DB 4; Pred. No. 2.1; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                   42;
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                                                                                         Length 2613;
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                                                                  Indels
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265

TTAAATAATTATCTTTTTCATTATCTGTACTTAAATATGT

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RESULT 7
US-08-480-604A-
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Patent No
Query Ma
Best Loc
Matches
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APPLICATION DATA:

FILING DATE: 16-MAR-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94104
COMPUTER READABLE FOI
MEDIUM TYPE: Flopi
COMPUTER: IBM PC (
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                          FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FITTING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07, FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION: NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                   FEATURE:
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                                                  480-
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CITY: SA
STATE: C
COUNTRY:
                                              NAME/KEY:
LOCATION:
480-604A-27
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Match 6.5%;
Local Similarity 58.0%;
Nes 58; Conservative
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                                                                                                                                                                                                                                                                             IOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION
                                                                                                           TOPOLOGY:
                                                                                                                                             LENGTH:
                                                                                                                                                                                                                   REFERENCE/DOCKET NUM
                                                                                                                     STRANDEDNESS
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SAN FRANCISCO
                                                                                                                                  nucleic
                                                                                                TYPE:
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UNITED STATES
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THALLEY, BRUCE
PADHYE, NISHA
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STAFFORD,
                                                           CDS
1..3888
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                                                                                                          linear
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PC compatible
FEM: PC-DOS/MS-DOS
FEM: PC-DOS/MS-DOS
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07-JUN-1995
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                                                                                                                                                base
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                                                                                                                                                                                                                      NUMBER:
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            Score
Pred.
 ore 32.8; DI ed. No. 2.6; Mismatches
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                         DB
   42;
                        Length
   Indels
                          3891;
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   0;
   Gaps
   0;
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RESULT 8
US-08-405-496A-27
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GENERAL INFORMATION:
                                                                                                             Matches
                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
-08-405-496A-2
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3891 base pairs
TYPE: nucleic acid
STEANDEDNESS: Acuble
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SEQUENCE C
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TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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FILING DATE: 02-DEC-
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OPERATING
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CITY: STATE:
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 TTAAC
                                                                                                           Similarity 58; Conserv
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PLICATION DATA:
DATE
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Application US/08405496A
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220 MONTGOMERY STREET, SUITE 2200
AN FRANCISCO
 AACATTCTTCCAAGATCAGTTGAATAAATTCTCTCAAATAATTTTGTAACTCCCT 266
                               AACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATATTTTTTAAATCTCACT 461
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YPE: Floppy disk
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04-DEC-1992
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                                                                                                          Score 32.8; DE Pred. No. 2.6; 0; Mismatches
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US-08-915-136-27
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US-08-915-13
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    Query
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                                                                                                                                                         REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 27:
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APPLICATION NUMBER: US
FILING DATE: 02-DEC-1S
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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FILING DATE: 16-MAR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 25-OCT-19
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
ADDRESSEE: MEDLEN
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                MOLECULE
                                                                    FEATURE:
                                                                                                                                               SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE:
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ZIP: 941
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CITY: STATE:
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    Match
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                                                                                TYPE:
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CALIFORNIA
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PADHYE, NISHA
FIRCA, JOSEPH R.
STAFFORD, DOUGLAS C.
STAFFORD, DOUGLAS C.
NVENTION: VACCINE AND A
NVENTION: PREVENTION OF
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O MONTGOMERY STREET,
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02-DEC-1993
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16-MAR-1995
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RESULT 11
US-09-244-796-17
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US-09-007-005-1
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TITLE OF INVENTION: SELECTION OF PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,00
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
                                                                                                     Sequence 1
Patent No.
GENERAL IN
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Matches 11
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ORGANISM: Art
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OTHER INFORMATION: n
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OTHER INFORMATION:
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No. 6258558
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Similarity 5.4%;
.1; Conservative 8
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Roberts, Richard W.
  NTION:
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1344
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SELECTION OF PROTEINS USING
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87; Mismatches
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FILE REFERENCE: 00786/35000,
FILE REFERENCE: 00786/35000,
CURRENT APPLICATION NUMBER: US/09/244,/>
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
CHARLIER FILING DATE: 1998-01-14
CHARLIER FILING DATE: 1998-01-14
                                                                                                              GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Hengartner, Michael

TITLE OF INVENTION: IDENTIFICATION AND CHA

TITLE OF INVENTION: GENE WHICH PROTECTS CE

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 01997/201005

CURRENT APPLICATION NUMBER: US/09/234,186

CURRENT FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: 07/898,933

EARLIER FILING DATE: 1992-06-12

EARLIER APPLICATION NUMBER: 07/927,681

EARLIER APPLICATION NUMBER: 08/288,295

EARLIER APPLICATION NUMBER: 08/288,295

EARLIER APPLICATION NUMBER: 08/288,295

EARLIER FILING DATE: 1994-08-10

EARLIER FILING DATE: 1994-08-10

EARLIER FILING DATE: 1997-02-19
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; LOCATION: (1)...(289)
; OTHER INFORMATION: n =
US-09-244-796-17
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US-09-234-186-1/c
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OTHER INFORMATION:
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ORGANISM: Artificial Sequence
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               Caenorrhabditis
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; LOCATION: (1)...(6559); OTHER INFORMATION: n = AUS-09-233-527-1
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; LOCATION: (1)...(6559)
; OTHER INFORMATION: n =
US-09-234-186-1
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APPLICANT:
TITLE OF IN
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CURRENT FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 07/898,933
PRIOR FILING DATE: 1992-06-12
PRIOR APPLICATION NUMBER: 07/927,681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/801,248
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
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FEATURE:
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al Similarity 52.2%;
72; Conservative
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ICATION NUMBER: 07/927,681

ICATION NUMBER: 07/927,681

ICATION NUMBER: 08/288,295

ICATION NUMBER: 08/288,295

ICATION NUMBER: 08/288,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: 1994-08-10
ATION NUMBER: 08/801,248
DATE: 1997-02-19
                                                                          GGTCGCTGCAGAA 6293
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US-08-471-033-39; Sequence 39, A
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MOLECULE TYPE:
PCT-US93-05651-1
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Patent No. 5//00:
Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.5%;
Best Local Similarity 52.2%;
Matches 72; Conservative
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                                                                                                       ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PC INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                         APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
                    APPLICATION NUMBER: US 0 FILING DATE: 09-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6311
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                             STREET:
CITY: Ha
CITY: Ha
COUNTRY:
APPLICATION NUMBER: US 08/218,018 FILING DATE: 23-MAR-1994
                                                                                                                                                                                                                         ADDRESSEE: Clbn 7 Skyline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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10532
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Desai, Nalini
Kostichka, N.
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Mullins,
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Michael
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                                                                                                                     Version
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Best Local S
Matches 74
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LENGTH: 1241 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   time
                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other DESCRIPTION: /desc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                -471-033-39
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                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 9..1238
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                         199
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completed: 1 ne : 63.6858
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TOPOLOGY:
                                                                                                                                                                                     59
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                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
                                                   CCAACCTGAGCAACAGCATCATCA
                                                                             CCCTTCACATCTTCAACGCCATCA
                                                                                                   CCGGCAGCTTCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGA 258
                                                                                                                   CTGAAATCATGCATGAGCAGATCTGCCCCCTGGAGGAGAAGACGAGCGTCTTACCGAATT 178
                                                                                                                                                        ACCAGC
                                                                                                                                                                                                         ch 6.4%;
Similarity 51.4%;
74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CE/DOCKET NUMBER: CGC 1
NICATION INFORMATION:
NE: 919-541-8582
919-541-8689
FOR SEO TO TO
                                                                                                                                                                                TCGAGTATCAGGAAGAAATGAAAGCCAACTACAGGGAAATGGCGAAGGAGCTTT 118
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             February
secs
                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                   /desc
                                                                                                                                                                                                                                                                    /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion sig removed as contained in pCIB5527"
                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
= "Synthetic DNA"
           2003,
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            09:06:22
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

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US-09-736-960-1
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FILE REFERENCE: 210121.466C3
CURRENT APPLICATION NUMBER: US,
CURRENT FILING DATE: 2001-06-
NUMBER OF SEQ ID NOS: 353
SOFTWARE: FastSEQ for Windows
SEQ ID NO 157
LENGTH: 1031
TYPE: DNA
ORGANISM: Homo sapien
US-09-876-889-157
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APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 3043
                                                 OTHER INFORMATION:
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APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OF TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
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R FILING DATE: 2000-04-11

OR FILING DATE: 2000-04-11

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OR TIME: 2000-04-11
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R APPLICATION NUMBER: US 60
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NT: Candia III, Albert Frederick
NT: Arbor Vita Corporation
F INVENTION: CLASP-4 Transmembrane Progression
FERENCE: 020054-000411US
F APPLICATION NUMBER: US/09/736,969A
F FILING DATE: 2000-12-13
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
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RENT FILING DATE: 2001-03-01
OR APPLICATION NUMBER: 60/186,126
OR FILING DATE: 2000-03-01
OR APPLICATION NUMBER: 60/190,479
OR APPLICATION NUMBER: 60/200,545
OR FILING DATE: 2000-04-27
OR APPLICATION NUMBER: 60/200,303
OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: 60/200,303
OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: 60/200,999
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: 60/202,084
OR APPLICATION NUMBER: 60/206,201
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: 60/206,201
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: 60/218,950
OR APPLICATION NUMBER: 60/223,416
OR APPLICATION NUMBER: 60/233,416
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OR APPLICATION NUMBER: 60/223,416
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Mannion, Jane
MANNION: COMPOSITIONS AND METHODS FOR THE DETECTION,
PENTION: HEMATOLOGICAL MALIGNANCIES
ACE: 2077.001200
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Publication No. US20020198362A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: HEMATOLOGICAL M.
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/79(
CURRENT FILING DATE: 2001-03-01
CURRENT FILING DATE: 2001-03-01
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NAME/KEY:
LOCATION:
OTHER INFO
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R APPLICATION NUMBER: 60/218,95
R FILING DATE: 2000-07-14
R APPLICATION NUMBER: 60/222,96
R APPLICATION NUMBER: 60/223,4
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R APPLICATION NUMBER: 60/20
R FILING DATE: 2000-04-28
R APPLICATION NUMBER: 60/20
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APPLICATION
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TYPE: DI
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                                                                                       PLICANT: Garman, Jonathan David
PLICANT: Candia III, Albert Frederick
PLICANT: Arbor Vita Corporation
TLE OF INVENTION: CLASP-5 Transmembrane PI
LE REFERENCE: 020054-000511US
RRENT APPLICATION NUMBER: US/09/736,960
RRENT FILING DATE: 2001-09-20
IOR APPLICATION NUMBER: US 60/160,860
IOR APPLICATION NUMBER: US 60/162,498
IOR APPLICATION NUMBER: US 60/162,498
IOR APPLICATION NUMBER: US 60/170,453
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R APPLICATION NUMBER: 60/200,779
R FILING DATE: 2000-04-28
R APPLICATION NUMBER: 60/200,999
R FILING DATE: 2000-05-01
R APPLICATION NUMBER: 60/202,084
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R APPLICATION NUMBER: 60/190,479
R FILING DATE: 2000-03-17
R APPLICATION NUMBER: 60/200,545
R FILING DATE: 2000-04-27
R APPLICATION NUMBER: 60/200,303
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APPLICATION NUMBER: 60/223,378
FILING DATE: 2000-08-07
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R APPLICATION NUMBER: US 60/182,296

R FILING DATE: 2000-02-14

R APPLICATION NUMBER: US 09/547,276

R FILING DATE: 2000-04-11

R APPLICATION NUMBER: US 60/196,267

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TON: CLASP-5 Transmembran
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LENGTH: 7215
TYPE: DNA
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APPLICATION 1999-10-29
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5. US20020102267A1
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CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
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NUMBER OF SEQ ID NOS: 583
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RESULT 15
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Best Local Similarity 57.4%;
Matches 66; Conservative
                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Haselbec
                APPLICANT:
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TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF
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FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-
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OTHER INFORMATION: n=a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IOR APPLICATION NUMBER: US/09/954,456
IOR APPLICATION NUMBER: US/60/233,617
IOR FILING DATE: 2000-09-18
IOR APPLICATION NUMBER: US/60/234,052
IOR FILING DATE: 2000-09-20
OR APPLICATION NUMBER: US/60/234,923
OR FILING DATE: 2000-09-25
OR APPLICATION NUMBER: US/60/235,134
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OR APPLICATION NUMBER: US/60/235,638

OR FILING DATE: 2000-09-26

OR APPLICATION NUMBER: US/60/235,711

OR FILING DATE: 2000-09-27

OR APPLICATION NUMBER: US/60/235,720

OR FILING DATE: 2000-09-27

OR APPLICATION NUMBER: US/60/235,840

OR APPLICATION NUMBER: US/60/235,840
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APPLICATION NUMBER:
FILING DATE: 2000-C
                                                                                                                                                                                                                                                                                                                                                                      TCGAAATAGTATGAATTTTAATATATACTTTTAAAGGGGTTAGGCAATGATGAAA
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Zyskind, Judith Wall, Daniel Trawick, John D. Carr, Grant
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SEQ ID NOS: 2276
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2000-09-27
IUMBER: US/60/235,863
                                         John D.
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; LOCATION: (1)...(696)
US-09-815-242-7900
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SEQ ID NO 7900
LENGTH: 696
TYPE: DNA
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Best Local
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
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NAME/KEY:
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completed
ne : 83.35
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R APPLICATION NUMBER: 60/191,078

R FILING DATE: 2000-03-21

R APPLICATION NUMBER: 60/206,848

R FILING DATE: 2000-05-23

R APPLICATION NUMBER: 60/207,727

R FILING DATE: 2000-05-26

R APPLICATION NUMBER: 60/242,578

R APPLICATION NUMBER: 60/253,625

R APPLICATION NUMBER: 60/253,625

R APPLICATION NUMBER: 60/257,931

R APPLICATION NUMBER: 60/257,931

R APPLICATION NUMBER: 60/257,931

PR APPLICATION NUMBER: 60/257,931

R APPLICATION NUMBER: 60/257,931
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                                                          CGTCGGT
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                                                                                                                                              TCTTCAACGCCATCAGTGGGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGT
                                                                                                                                                                          TGCATGAGCAGATCTGCCCCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACA 187
                                                                                                                     AATGAA
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Similarity 52.3%;
81; Conservative
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(u, H. Howard
ENTION: Identification of Essential Genes
ENTION: Prokaryotes
DE: ELITRA.011A
49
                                                         TCAGCTGGGCCAGATCCTCGGCCCGCGTG
                                                                                       TCGTGTGATTACATCTCATGGCCCGTGTG 282
                                                                                                                  AGGCGGCGACCTGAACTACGACGTCGTCATCGCTTCCCCGGATGCCATGCGTGT 368
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February
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            2003, 09:15:32
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                                                                                                                                                                                                                                      Score 36.6; DB 10;
Pred. No. 0.25;
0; Mismatches 74;
                                                          403
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                  Length 696;
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